

us-09-509-234c-50.rge

Fri Jun 21 08:38:25 2002

1 1284 100.0 1284 6 A97494
2 1233 96.0 1254 1 AF099966
3 628 48.9 1343 1 SHV12874
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6 622.6 48.5 1263 1 SSU66880
7 622 48.4 1257 1 AFI44663
8 613.8 47.8 1283 6 A97490
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23 585.4 45.6 1263 1 AFI44661
24 584.8 45.5 1280 6 A97486
25 584.6 45.5 1260 1 AF099963
26 579 45.1 4434 1 AF269697
27 579 45.1 4434 6 AX145015
28 578.4 45.0 1263 1 AF099965
29 577.4 45.0 1877 1 SEU23713
30 574.4 44.7 1257 6 I32344
31 554.2 43.2 1179 6 AX141471
32 537.6 41.9 1328 6 A97445
33 346.8 27.0 1805 1 AF093750
34 346.8 25.7 6528 1 SSU66883
35 324.4 25.3 1551 1 AF106849
36 324.4 25.3 297850 1 AP003137
37 324.4 25.3 341350 1 AP003365
38 324 25.2 347235 1 AP003361
39 322.8 25.1 2558 1 AB000222
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44 315 24.5 54064 2 AC090968
45 301.2 23.5 1254 6 AX141473

ALIGNMENTS

RESULT 1
LOCUS A97494 1284 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 50 from Patent WO9916780.
ACCESSION A97494
VERSION A97494.1 GI:6780840
KEYWORDS Staphylococcus sciuri.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1284)
AUTHORS Gala, J. and Vannuffel, P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9916780-A 50 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES
source location/Qualifiers
1..1284
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CDS
1..1233
/note="unnamed protein product"

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:13:00 ; Search time 12428.6 Seconds
(without alignments)
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Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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Matches 1284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
AF099966      1254 bp      DNA      linear      BCT 02-NOV-1998
LOCUS      Staphylococcus sciuri factor essential for methicillin resistance
DEFINITION      FMA (fema) gene, complete cds.
ACCESSION      AF099966
VERSION      AF099966.1 GI:3820631
KEYWORDS      Staphylococcus sciuri.
SOURCE      Staphylococcus sciuri.
ORGANISM      Bacteria: Firmicutes: Bacillus/Clostridium group;
      Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE      1 (bases 1 to 1254)
AUTHORS      Vanhuffel,P., Heusterspreute,M., Bouyer,M., Philippe,M. and Gala
      J.-L.
TITLE      Molecular characterization of fema from Staphylococcus hominis,
      Staphylococcus saprophyticus and Staphylococcus haemolyticus and
      fema-based discrimination of Staphylococcal species
      Res. Microbiol. (1998) in press
AUTHORS      Vanhuffel,P., Heusterspreute,M. and Gala,J.-L.
TITLE      Direct Submission
JOURNAL      Submitted (21-OCT-1998) LBCM, UCL, Clos Chapelle-aux Champs
      30/3046, Bruxelles 1200, Belgium
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Best Local Similarity 100.0%; Pred. No. 6.1e-176;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 82 GSPAATTATGAAATTAACAAATCATGAAGTACTTCAACACATTTAGTAGGGTCAAGAT 141
Qy 121 aatcaagtggaattagctgctgtctgtttaaacaagtgaccagttatgaagaattt 180
Db 142 AATCAAGGTGAAGTATTAGTGGCTGTCTGTTAACAAAGTGTACCAAGTATGAAGAAATTT 201
Qy 181 aattactttactcaaatagagagaccagtaagtgtatgatatgacacaaagaactttgac 240
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Qy 241 tttttttaaagaatactgtagctattttaaagaattttaaagaatttcttttagaattc 300
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Qy 661 agattcaataactttgaaatgaagattccttttagcatatataagactttgaaacttac 720
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RESULT 3
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DEFINITION Staphylococcus hominis fema gene.
ACCESSION Y12874
VERSION Y12874.1 GI:2462667
KEYWORDS fema gene.
SOURCE Staphylococcus hominis.
ORGANISM Staphylococcus hominis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1343)
AUTHORS Vannuffel, P.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1343)
AUTHORS Vannuffel, P.
TITLE Direct Submission
JOURNAL Submitted (30-APR-1997) P. Vannuffel, University of Louvain Medical
School, Laboratoire de Genetique Moleculaire, UCL-GENO-5225, Avenue
E. Mounier 52, Brussels, 1200, BELGIUM
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Query Match	48.98;	Score 628;	DB 1;	Length 1343;
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RESULT	4				
LOCUS	A97496	1343 bp	DNA	linear	PAT 26-JAN-2000
DEFINITION	Sequence 52 from Patent WO9516780.				
ACCESSION	A97496				
VERSION	A97496.1	GI:6780842			
KEYWORDS	.				
SOURCE	Staphylococcus hominis.				
ORGANISM	Staphylococcus hominis.				
	Bacteria; Firmicutes; Bacillus/Clostridium group;				
	Bacillus/Staphylococcus group; Staphylococcus.				
	1 (bases 1 to 1343)				
REFERENCE	Gala, J. and Vannuffel, P.				
AUTHORS	GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND				
TITLE	DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS				
JOURNAL	Patent: WO 9516780-A 52 08-APR-1999;				
	GALA JEAN LUC (BE); UNIV LOUVAIN (BE)				
FEATURES	Location/Qualifiers				
source	1..1343				

CDS

Location/Qualifiers
1. .1343

BASE COUNT	544 a	161 c	218 g	420 t
ORIGIN				

Query Match	48.88;	Score 626.4;	DB 6;	Length 1343;
Best Local Similarity	70.08;	Pred. No. 5.2e-85;		
Matches 859;	Conservative 0;	Mismatches 366;	Indels 3;	Gaps 1;

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QY 127 ggtgaagattatagctgctgtctgttaacaagtgctaccagtttatgaagaaatttaattac 186
Db 211 AATGAAGTCATGCTGCTGTGTATGCTAACGTCTGTACCCGTTATGAAATTTTAAATAT 270
QY 187 ttctactcaaatagaggaccagtaagtattatgacacaaagaactgttgacttttc 246
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QY 247 tttaagaagaatcgtagctatttaaaagtataaaggattattcttttagaatcgatcct 306
Db 331 TTTAACGAATTAAGTAATATTTAAACAAACAACTGTTTATATGTTAGCTATAGACCT 390
QY 307 tactgcccataactcaactaagatgatgagcaattataaaaaatcattcaaccgtgat 366
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Db 511 GATCCAATATTACAAATTCGGTTCCTCATTAGTTTAAATTTAAAGGATAAAACTGCTAAA 570
QY 487 acgctctcaagaacatgagcagtttaagaagaaagaataactaaaaagtccaataaat 546
Db 571 GATGTTTAAATGGAATGGATGTTTACGAAAAAGAAATTAATAAAAGTCCAAAAAAT 630
QY 547 ggtgttaaagtcgtttctctatcaaatgaatgaaatgcgcatattccgtcaattatgaa 606
Db 631 GGTGTTAAAGTAAGATTTCTTACTAAGAGAATTTACCTATTTTCAGATCATTATGGA 690
QY 607 gatactacagagaagaagatttcaacgatcggtggcgatgactcttattacaatagatta 666
Db 691 GATACATCAGACGATAAAGAAATTTCTGTATGAGAGAGATAGTTTACTATAATCGATTT 750
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Db 1291 ACAACACTTAAAAAATTTAAAAAGAGAT 1318
RESULT 5
LOCUS A97497 1371 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 53 from Patent WO9916780.
ACCESSION A97497
VERSION A97497.1 GI:6780844
KEYWORDS
SOURCE
ORGANISM Staphylococcus saprophyticus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Staphylococcus group; Staphylococcus.
REFERENCE
AUTHORS Gala, J. and Vannuffel, P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9916780-A 53 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES
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Query Match 48.8%; Score 626; DB 6; Length 1371;
Best Local Similarity 69.08; Pred. No. 5,9e-85;
Matches 887; Conservative 0; Mismatches 395; Indels 4; Gaps 2;
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Db 146 GAAATATGAATTTGAAATTTGCAAGAAAGTACAGAAACACACCTAGTAGTATTAAGAATA 205
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Db 326 ACTTCTTTAACGAATTAGCAAAATATGAAAAAACAATAATGCCTTATATTACGAGTAG 385
QY 302 atccttactgcatatcaactaagaagatcatgatggcaatattataaaaaaatcatcaacc 361
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 QY 422 gtccaccaacatatacaaatgaattgagcattcgtctcattgattgaagatcagacg 481
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 Db 806 ATATACAGATTTAAAGCTGAAACGGAATTTATGATGATGATGATGATGATGATGATGAT 865
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 QY 1258 tagataatataatataatataatataatataatataatataatataatataatataat 1283
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RESULT 6
 SSU66880 1263 bp DNA linear BCT 25-APR-1997
 LOCUS SSU66880
 DEFINITION Staphylococcus simulans fema (fema) gene, complete cds.
 ACCESSION U66880
 VERSION U66880.1 GI:1762961
 KEYWORDS

SOURCE Staphylococcus simulans.
 ORGANISM Staphylococcus simulans
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1263)
 AUTHORS Thumm G. and Goetz F.
 TITLE Studies on polysaccharide processing and characterization of the
 lysostaphin immunity factor (Lif) of Staphylococcus simulans biovar
 staphylophilus
 JOURNAL Mol. Microbiol. 23 (6), 1251-1265 (1997)
 MEDLINE 97260121
 REFERENCE 2 (bases 1 to 1263)
 AUTHORS Thumm G. and Goetz F.
 TITLE Direct Submission
 JOURNAL Submitted (13-AUG-1996) Mikrobielle Genetik, Universitaet
 Tuebingen, Waldhauser Strasse 70/8, Tuebingen 72076, Germany
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 BASE COUNT 470 a 191 c 241 g 361 t
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Query Match 48.5%; Score 622.6; DB 1; Length 1263;
 Best Local Similarity 69.5%; Pred. No. 26-84;
 Matches 860; Conservative 0; Mismatches 374; Indels 3; Gaps 1;

QY 1 acactggaatttgaagcttttcaataataatgctgacgcgactttatcaacaagcagta 60
 Db 22 ACAGCTGAATTTGAGATTTTACAGATTAATGCGATATAGCATTTTACACAATAGTA 81
 QY 61 ggtattatgaatataaacaatcgtgaaggtactcaacaacttgtaggggtcaagaat 120
 Db 82 GGCACATPATGATGAAAGTTGCAAGAGTACAGAAACATCTTGCGGGTGAAGAC 141
 QY 121 aatcaagtgaaatattagctgctgctgtttaaagaagtgatccaggtatagaat 180
 Db 142 AAAGATNCAATGTCTTTCACAGATGTTTACTTACAGCTGTCAGTATATAATTTCTT 201
 QY 161 aattactttactcaaatagagacgaatagattatgacaacaagaagactgttgac 240
 Db 202 AAATATTTCATTCACAAACGCGTGCATGATTTATGATTAATTAAGAAATGTGTCAT 261
 QY 241 ttttcttaagaacatcgtagcattataaagaattataaagaattatctcttagaact 300
 Db 262 TACTTCTTTAGAGATTTAAAGCATATGTTAAACAAATGATTTACTTAAAGATA 321
 QY 301 gatccttactgcatatcaactaagaatcagatgagcaatataataaataatcacaac 360
 Db 322 GATCATATTTCACATATCAATACCGTACCATGATGATGATGATGATGATGATGATGATGAT 381
 QY 361 cgtatggtttaaataaacaattgaatcattaggtatgacccaaggtccacaact 420

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Db 448 GATCCATATACAGTAAGACACATTCAGTATTGATTTAAAGSTAAACTGCAAAA 507

QY 487 acgctcacaagacatggacagtttaagaanaaataactaanaaaagttcaaaaaat 546

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QY 547 ggttaagttcgtttctatcctaagaatgaatgcgattatccgcacattatgaa 606

Db 568 GGTGGAAGAGTTAATTTCTATACAGAGATGAATTAACGATTTCCGATCATTCATGGA 627

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Db 688 AAGCATTCAAGATGCCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 747

QY 724 ccacatagaagaagaacatgaacatacaacaaagatctgcaaaagctgaagaagat 783

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QY 844 agagaagaagaagaagaacatgaacatacaacaaagatctgcaaaagctgaagaagat 903

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QY 1024 attaatacagttatgaacatacaacatgaacatacaacaaagatctgcaaaagctgaagaagat 1083

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RESULT 8

LOCUS A97490 1283 bp DNA linear PAT 26-JAN-2000

DEFINITION Sequence 46 from Patent WO916780.

ACCESSION A97490

VERSION A97490.1 GI:6780836

KEYWORDS

SOURCE

ORGANISM

Staphylococcus capitis.

Staphylococcus capitis

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Staphylococcus.

REFERENCE

1 (bases 1 to 1283)

Galal, J. and Vanunite, P.

GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND

DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

Patent: WO 91/6780-A 46 08-APR-1999;

JOURNAL

GALAL JEAN LUC (BE); UNIV LOUVAIN (BE)

FEATURES

Location/Qualifiers

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BASE COUNT 484 a 170 c 224 g 405 t

ORIGIN

Query Match 47.8%; Score 613.8; DB 6; Length 1283;

Best Local Similarity 68.6%; Pred. No. 4.1e-83;

Matches 879; Conservative 0; Mismatches 392; Indels 10; Gaps 2;

QY 7 gaattgaagctttacaataaatgcccgaacgagatttacaagaagcagtagtaat 66

Db 10 GAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 69

QY 67 tatgataaagaacatctgaagcttcaacacatttagagggtcaagaataatcaa 126

Db 70 TATGACTTAAGTTGCTGAAGTACGATTCACATCTCTAGAGATTAATAAATGAC 129

QY 127 ggtgaagattagctgctgctgttaacaagtgaccagtttagaagaattatc 186

Db 130 AACCAAGATTTGACGAGATTTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 189

QY 187 tttaactcaatagaagcaggaatgattatgaacaaagaagcttgaactttc 246

Db 190 TTTTACTCAATTCGGGGCCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 249

QY 247 tttaagaagaatcgagacttaaaagaattaaagattatcttgaactcga 306

Db 250 TTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 309

QY 307 tacttgcatacaactgaagaagatgagatgagcaataataaataatcaatcgaactg 366

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Db 370 TGGTTTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 429

QY 427 caaccaatcacaactatagatgagcactgctgactgattagaagaatgagcgaag 486

Db 430 CATCTTATCTTAAGTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 489

QY 487 acgtcacaagaagaatgagcagtttaagaagaagaatgaactcaaaagctcaaaaaat 546

Db 490 GATGTAATCAAGATGATGATGATTAAGAAACGTAATTAATTAATTAATTAATTAAT 549

QY 547 ggttcaagttcgtttctatcctaagaagaatgagcagatatacgcataatgagaa 606

Db 550 GGTGTCAAGTCCGTTCTTATCCAGAGATTAATTAATTAATTAATTAATTAATTAAT 609

QY 607 gatactacaagaagaagaattcaacagtcgtagcagtaactctatcaataagatta 666

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RESULT 10
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 LOCUS SSY12875
 DEFINITION Staphylococcus saprophyticus fema gene.
 ACCESSION Y12875.1 GI:2462696
 VERSION Y12875.1 GI:2462696
 KEYWORDS fema gene.
 SOURCE Staphylococcus saprophyticus.
 ORGANISM Staphylococcus saprophyticus
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1350)
 AUTHORS Vannuffel, P.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1350)
 AUTHORS Vannuffel, P.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-1997) P. Vannuffel, University of Louvain Medical
 School, Laboratoire de Genetique Moleculaire, UCL-GENO-5225, Avenue
 E. Mounier 52, Brussels, 1200, BELGIUM
 COMMENT Y12875 incorrectly cited in: Science: 276: 2054-2057 (1997).
 FEATURES
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 Best Local Similarity 68.9%; Pred. No. 1,3e-82;
 Matches 852; Conservative 0; Mismatches 381; Indels 3; Gaps 1;

Qy 2 cacttgaatttgaagcctttacaataaatgccgtaagcggatttacaagaagcagtag 61
 Db 87 CAAAGAGTTCGGTGCATTTACGATTAATAATGCCGAATAGTCATTTTACGCAATGTTG 146
 Qy 62 gtaattatgaataaacaatctgaagttactcaacaattagtaggggtcaagata 121
 Db 147 GAAATATGAATGAAATTTGCAAAATTCAGAAATACAGAAACACCTAGTAGTATTAAGAATA 206
 Qy 122 atcaagtgtaagattatagctgctgctgttaacaagtgtaacagttcagaataatta 181
 Db 207 ATGATATGAAGTATTTGCAGCATGTTTACTACAGCTGTTCTGTATGAAATTTCTTCA 266
 Qy 182 attacttttactcaaatagaagaacagtaagtattatgcaacaagaagacttttgact 241
 Db 267 AGTATTTTATCCAAATAGAGGTCAGCATAGATTTGAAATTAAGACCTGATACAT 326
 Qy 242 ttcttcaagaatcgtgagctatcttaaaaagttaagaagattatcttttagatcg 301
 Db 327 ACTTCTTTACGAATTTAGCAAAATATGTAAATAAACATTAATGCTTATTTTACAGATAG 386
 Qy 302 atoccttacttcacatcaactaagaatcagatcagtgcaatattaaataatcattcaac 361
 Db 387 ATCCATATCTTGCTTATCAATATCGTATCATGATGATGAAATGCGGGTGC 446
 Qy 362 gtgagtttacttaataaacaatttgaaatcattaggtatgaacacaaagcctcaaaactg 421
 Db 447 AGCATTTGATTTTGATTAATGAATGAACCACTCGTTATTAACATGAAGGTTTAACTG 506
 Qy 422 gtccacccaataatcaatattagatgagcattcgtactgattatagaagaatgagcag 481
 Db 507 GCTTTCACCAATACCTCAATTAATAGATTCATTCGTTTGTATTAAGTCGGMAAATG 566
 Qy 482 aaaaagcgtcatcaagaacatgacagtttaagaagaagaataactaaagaatcaca 541
 Db 567 CTAAAGACGACTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
 Qy 542 aaaaatgtttaaagtcgttttctatcaagaatgaatgcgaatcttcgcaattta 601
 Db 627 AAAATGGTGAAGAAATGAATTTTATAGTGAATGATGATGATGATGATGATGATGATGAT 686
 Qy 602 tggagaatctacagaagaagaagatttcaagatcgtgagcagttatctatcaata 661
 Db 687 TGGAAAGTACTTCTGAAACCAAGGATTTTACATAGATGATGATGATGATGATGATGAT 746
 Qy 662 gattaataactttgaaa--tgtaagaattccttiagcatatataagactttgaact 718
 Db 747 GGTTAATATTTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 806
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 Db 807 ATATACAGCAATTAAGCGTGAACCGCAAGTATTAAGTAAATTAATTAATTAACAGCTTA 866
 Qy 779 aagattagaagaagaacagataataaagaagaatgaataaataatagacaactttaa 838
 Db 867 AGGATATTAAGAAAAAGCCGAAATTAATAAAGCTATTAATAAATAAATAATTAAGAAC 926
 Qy 839 aacaaagaagaagaatgaagtaaatatagaagaagcattcaactacaagaagaatg 898


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OY 904 acattacaatagcagctggtttcttattatattacattgaagttgatatatgca 963
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Db 928 GAATTAACCTTTTCAGCTGATATTTCTTCAATTAACCGTTGAAGTGTATATACGA 987
OY 964 ggtgttcacatgcaatgaatctgacttgcagtgagttatgcaatcagtggaag 1023
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OY 1024 attaaacacggttaatatcaacattgaccggttaacttctatgcatcagcgagac 1083
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Db 1048 ATAAACATGCTTTAGAACATGCAATTAACCGTTATATTTTATGAGTATGCGGAGC 1107
OY 1084 ttctcaagaagatgcacctgattgtgcgttattatattaaagaagttacatgcagat 1143
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Db 1108 TTCACTGAAGCGTGAAGATGATAGAGTATTAAGTCAAAAAGCGTATATATGCTGAT 1167
OY 1144 gttatgaatatattgtgattcgttataaccaattataaaccggtacaaagcatat 1203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1168 GTTATTGAATGTAGTGTGATTTTATCAAGCCAAATCAATTAACCTATGATGCAATCTAT 1227
OY 1204 acaacacataaaagaattataaaaa 1229
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Db 1228 AACGACCTTAAAGATTAAAGAAATA 1253

RESULT 12
SAFE MA 3446 bp DNA linear BCT 19-JUL-1995
LOCUS S.aureus factor essential for expression of methicillin resistance
DEFINITION (fema) gene, complete cds, and trpA gene, 3' end.
ACCESSION X17688.M23918
VERSION X17688.1.GI:46579
KEYWORDS fema protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 3446)
AUTHORS Berger-Bachl,B., Barberis-Maino,L., Strassle,A. and Kayser,F.H.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3446)
AUTHORS Berger-Bachl,B., Barberis-Maino,L., Strassle,A. and Kayser,F.H.
TITLE FemA, a host-mediated factor essential for methicillin resistance
JOURNAL in Staphylococcus aureus: molecular cloning and characterization
MOL. GEN. GENET. 219 (1-2), 263-269 (1989)
MEDLINE
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
COMMENT by B.Berger-Bachl, 11-APR-1989.
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BASE COUNT 1281 a 448 c 617 g 1100 t
ORIGIN

Query Match 46.9%; Score 602.2; DB 1; Length 3446;
Best Local Similarity 68.1%; Pred. No. 1.8e-81;
Matches 872; Conservative 0; Mismatches 398; Indels 11; Gaps 2;

OY 7 gaattgaacgttttacaataaattgcgcagcatatttacaagaacgagtgat 66
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Db 643 GAGTTTGCTGCTTACAGATAGCATAGCATATTCACCCAAAGTGTGGCCAC 702
OY 67 tatgaataaaacatctgaagtgactcaaccatttggtgggtgaagaataatca 126
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Db 703 TATGAGTTAAAGCTTCTGAAGTTATGAACACATTGTGGGAATTAACAAAT 762
OY 127 ggtgaagattagtcggtctgttcaacaagttacacgattgaagaataattac 186
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Db 127 TATTTATCAATTCGCGGTCACGATGATTATGAATGAACGTCGACCTTTTC 882
OY 187 tttaactcaatagagaccagtaatgattatgaacaacaagaactgttgactttc 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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OY 247 tttaagaacatcgtagcattttaaaagttaaaagattatcttgaagtcgaccc 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 883 TTTTATGAATTAACAAATATGTAAACATCGTTGTCTATACCTACATATGCA 942
OY 307 tactgcacatacaatgaagatgcatctgacttattgaagaattggaagatggaag 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 943 TATTTACATATCAACTCTTGAATCATGATGCGGAGATFACAGATATGCTGTAAT 1002
OY 367 ggttaaatlaacaattgaatcaatgattatgaacaacaagaagcttcaacatg 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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OY 427 caccacatacatcaaatgaatgcatctgacttattgaagaattggaagatggaag 486
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Db 1063 GATCCTGTCTACAAATTCGTTATCACTCAGTGTATGATTTTAAACATGACAT 1122
OY 487 acgcatacaagaacatgacagtttaagaanaagaataactaaagaattcaaaaat 546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1123 GACATCATTAATAAATATGATGAGCTTAGAAAACAAACAGAAAAGAT 1182
OY 547 ggtgttaaatgcttttctatcaatgaagaatgacgcgatatcgcgttaatttga 606
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BASE COUNT	458 a 208 c 258 g 342 t		
ORIGIN			
Query Match 46.9%; Score 602; DB 1; Length 1266;			
Best Local Similarity 68.8%; Pred. No. 2.4e-81;			
Matches 843; Conservative 0; Mismatches 380; Indels 3; Gaps 1;			
Qy	7	gaattgaagcttttacaataaataacgcgtacgcgtacgtttttacacacagcagtagtaat	66
Db	28	GAATTCGGTGGCTTCCACGGATAGTATGCCATACAGCCATTTTACGCAANTGGTAGGGAAC	87
Qy	67	tatgaataaaacacatcgaagctacttcaacacattagtaggggtcaagataataca	126
Db	98	TACGAGCTTAAAGTGGCAGAGGCTGCGAACAACATCTCGTGGTATTAAAGATAATCAA	147
Qy	127	ggtgaagtattagtcgctgtctgttaacaagtgctaccagtgctatgaagaatttaattac	186
Db	148	ACCACAGTATTACCTGCTGTTTATTAACTGCGGTACCAGTACATGAAAGTGTCAAAAT	207
Qy	187	ttttactcaaatagagaccagtaattaggtattgacacaaagaactgttgactttttc	246
Db	208	TTTTATACGAATCGCGACCTGTGATGGATTATGAGAACCAAGAACTCGTTCATTCTTT	267
Qy	247	tttaaaagaatcgtgagctatttaaaagttataaaggattattcttttagaatgatcct	306
Db	268	TTTATGAAGTACGCAAAATATGTAAATAAATAACAATGCAATGATATGTAAGAGTCGACCCG	327
Qy	307	tacttgcctatcaactaagaagatcatgatggcaattataaaataatcaattcaaccgtgat	366
Db	328	TACTTGCCTCAATGTTAAACAGTAATCATGATGGTGAAGTGATTGAACGATTCCAAATGAT	387
Qy	367	ggtttaataaacaatttgaaatcattaggtattgaacacacacagcgttcacacgtgttc	426
Db	388	TGGTCTCTTGACAAAATGCGCAACTCGGGTTTGAACACCAAGGCTTTTACACAGGGATT	447
Qy	427	caccacatacataaatttagctgctattctgctattttagaagaattgagcagaagaag	486
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Qy	487	acgctcatcaagaacatggacagtttaagaagaagaataactaaaaaagtcaaaaaaat	546
Db	508	GATATACGAAACAATATGGATAGTTTGAAGAGCGAAATACGAAAGTGCAGAAAAT	567
Qy	547	ggtgtaaatgctgtttttctatcaaatgaatgaatgcgatattccgtcaatttttgaa	606
Db	568	GGTGTGAAGTGCCTTTTGGGATGAGATGAGTACATATTTTACGCTCGTTTATGAA	627
Qy	607	gatactacagagaagaagatttcaacgacgtgctgacgtactcttattaccatagatta	666
Db	1243	GATACGTCAGAAATCAAAGCTTTTGTGATCGTGTGATGACAAATTTTACTACAAATCGCTTA	1302
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Qy	724	cccaatttgaaaaagacatgaacatacaaaagatttgcataaaagctgaaagaag	783
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Db	1603	GGTGTACATCAATCAATCATCTCGTCATTTTCCGGAAGTTATGCAAGTCAATGGGAATG	1662
Qy	1024	ataataacgcttagatcacacacattgacgcttataacttctatgctatgctacgaggac	1083
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Qy	1084	ttctcagaagatgcacctgatgttgcgttattataaataaaaggttacaatgcagat	1143
Db	1723	TTTACAGAAGATGCTGAAGATCTGCTGTAGTTAAATTCAAAAGAGTTCAATGCTGAA	1782
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Db	1783	ATTATGTAATGTTGTTGACTTTTATTAACCAATTAATAACCTGTTTACGACGATAT	1842
Qy	1204	acacactaaaaagattataaaaaataaatgatatttctcagtaagaaggggaattagata	1263
Db	1843	ACCGCACTTAAAGATTAAAGACAGA-----ATTTTGAAGAGGAATATATCAA	1894
Qy	1264	atatgaattttacagatttaa	1284
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RESULT 13			
AF144662			
LOCUS			
DEFINITION			
Staphylococcus intermedius factor essential for methicillin resistance (femA) gene, complete cds.			
ACCESSION			
AF144662			
VERSION			
AF144662.1 GI:4929300			
KEYWORDS			
SOURCE			
ORGANISM			
Staphylococcus intermedius.			
Staphylococcus intermedius			
Bacteria; Firmicutes; Bacillus/Clostridium group;			
Bacillus/Staphylococcus group; Staphylococcus.			
REFERENCE			
1 (bases 1 to 1266)			
Vannuffel,P., Heusterspreute,M. and Gala,J.-L.			
Cloning and characterization of femA genes from Staphylococci species			
JOURNAL			
Unpublished			
REFERENCE			
2 (bases 1 to 1266)			
Vannuffel,P., Heusterspreute,M. and Gala,J.-L.			
AUTHORS			
Direct Submission			
TITLE			
Submitted (21-APR-1999) LBCM, UCL 3046, Cios Chapelle-aux-Champs,			
JOURNAL			
30, Bruxelles 1200, Belgium			
FEATURES			
Location/Qualifiers			

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QY      427 caaccaatacatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 486
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QY      607 gatacctcagaagaagaagcttgaagcttgaagcttgaagcttgaagcttgaagcttga 666
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RESULT 14
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DEFINITION Sequence 48 from Patent WO9916780.
ACCESSION A97492
VERSION A97492.1 GI:6780838
KEYWORDS
SOURCE
ORGANISM
Staphylococcus schleiferi.
Staphylococcus schleiferi.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
1 (bases 1 to 1297)
Gala, J. and Vannuffel, P.
GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
TITERS FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
Patent: WO 9916780-A 48 08-APR-1999;
JOURNAL
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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CDS

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 DEFINITION protein fema (fema) gene, complete cds.
 ACCESSION AFI45333
 VERSION AFI45333.1 GI:5565908
 KEYWORDS Staphylococcus cohnii subsp. urealyticus.
 SOURCE Staphylococcus cohnii subsp. urealyticus
 ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1260)
 AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
 TITLE Cloning and characterization of fema genes from Staphylococci species
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1260)
 AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
 TITLE Direct Submission
 JOURNAL Submitted (23-Apr-1999) LBCN, UCL 3046, Clos Chapelle Aux Champs, 30, Bruxelles 1200, Belgium
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 CDS

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Page 16

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Fri Jun 21 08:38:26 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:46:39 ; Search time 1139.49 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	626	48.8	1371	AA37805	Staphylococcus sap
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4	613.8	47.8	1283	AA37801	Staphylococcus cap
5	601.6	46.9	1297	AA37802	Staphylococcus sch
6	595.6	46.4	1295	AA37800	Staphylococcus xyl
7	594.2	46.3	1305	AA37798	Staphylococcus hae
8	584.8	45.5	1280	AA37799	Staphylococcus lug
9	579	45.1	4434	AAH54373	S. epidermidis gen

10	574.4	44.7	1257	15	AA078141	Staphylococcus epi
11	554.2	43.2	1179	22	AAH52400	S. epidermidis ope
12	537.6	41.9	1328	20	AA37797	Staphylococcus sp.
13	330.2	25.7	658	21	AAZ49723	Staphylococcus sim
14	322.4	25.1	1470	20	AAZ22843	Staphylococcus aur
15	322.4	25.1	1470	20	AAZ19882	Staphylococcus aur
16	319.2	24.9	1245	23	AAH51125	Staphylococcus aur
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18	304.2	23.7	3821	18	AAV74615	Staphylococcus aur
19	301.2	23.5	1251	15	AAQ74775	Staphylococcus epi
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21	287.4	22.4	2453	22	AAH55015	S. epidermidis gen
22	259	20.2	1260	20	AAH07088	Staphylococcus aur
23	259	20.2	1260	20	AAH07091	Staphylococcus aur
24	254.2	19.8	1257	23	AAH51636	Staphylococcus aur
25	254.2	19.8	1260	23	AAH54419	Staphylococcus aur
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28	216.2	16.8	453	22	AAH08009	Staphylococcus aur
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30	194	15.1	410	21	AAZ26855	Essential Staphylo
31	194	15.1	410	22	AAH08006	Staphylococcus aur
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33	151.8	11.8	420	20	AAH89751	Synthetic DNA frag
34	149.4	11.6	795	23	AAH50908	Staphylococcus aur
35	147.4	11.5	514	18	AAH80799	Staphylococcus aur
36	146	11.4	1221	18	AAV74940	Essential Staphylo
37	139.6	10.9	400	21	AAZ26853	Staphylococcus aur
38	139.6	10.9	400	22	AAH08004	Staphylococcus aur
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41	106.8	8.3	10194	20	AAH13028	C. glutamicum SRT
42	104	8.1	289	18	AAV75592	Enterococcus faeca
43	102.8	8.0	1281	23	AAH52835	Enterococcus faeca
44	95.2	7.4	158	18	AAV76848	Staphylococcus aur
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ALIGNMENTS

RESULT 1
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ID AA37803 standard; DNA; 1284 BP.
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AC AA37803;
XX
XX 09-JUL-1999 (first entry)
DT Staphylococcus sciuri FemA DNA.
DE
XX
XX FemA; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine, ss.
XX Staphylococcus sciuri.
OS
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FT FT /note= "partial sequence, no start or stop codon"

WO9916780-A2.

XX 08-APR-1999.
XX 28-SEP-1998; 98WO-BE00141.
XX 26-SEP-1997; 97EP-0870146.
XX (BENA-) BELGTAN MIN NAT DEFENCE.
XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.

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us-09-509-234c-50.ing

PI Gala J. Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB: AAY08220.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 25; Fig 11a-b; 48bp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SO Sequence 1284 BP; 518 A; 181 C; 215 G; 370 T; 0 other;

Query Match 100.0%; Score 1284; DB 20; Length 1284;
 Best Local Similarity 100.0%; Pred. No. 2,5e-220;
 Matches 1284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 1081 gacttctcagaagatgcactgattgttgcttattataatttaaaaaggttacatgca 1140
 DB 1081 gacttctcagaagatgcactgattgttgcttattataatttaaaaaggttacatgca 1140
 QY 1081 gacttctcagaagatgcactgattgttgcttattataatttaaaaaggttacatgca 1140
 DB 1081 gacttctcagaagatgcactgattgttgcttattataatttaaaaaggttacatgca 1140
 QY 1141 gatgtttatgaatatattggtgatttcgttaacaacatataaacagcgtcacaaaga 1200
 DB 1141 gatgtttatgaatatattggtgatttcgttaacaacatataaacagcgtcacaaaga 1200
 QY 1201 tatcaacacataaaaagattataaaaataaagattttcaagtaagagagatttag 1260
 DB 1201 tatcaacacataaaaagattataaaaataaagattttcaagtaagagagatttag 1260
 QY 1261 ataataagaatttacaagttaa 1284
 DB 1261 ataataagaatttacaagttaa 1284

RESULT 2

AAK37805 standard; DNA: 1371 BP.

ID AAK37805;

AC AAK37805;

DT 09-JUL-1999 (first entry)

DB Staphylococcus saprophyticus fema DNA.

XX Fema: identification; detection; therapy; infection; femB;

XX amplification; genotyping; gram-positive bacteria; vaccine; ss.

XX Staphylococcus saprophyticus.

XX Location/Qualifiers

XX Key 64..1326

XX CDS /tag= a

XX W09916780-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98MO-BE00141.

26-SEP-1997; 97EP-0870146.
(BENA-) BELGIAN MIN NAT DEFENCE.
(UYLO-) UNIV CATHOLIQUE LOUVAIN.
Gala J, Vannuffel P;
WPI: 1999-287521/24.
P-PSDB: AAY08222.
New Staphylococcus-specific oligonucleotides
Claim 29; Fig 13; 48pp; English.
This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus femA nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various femA sequences which are specific to known or unknown Staphylococci species. Since the femA sequence is similar to the femB sequence, the oligonucleotides can also be used for the molecular genotyping of femB genes of different Staphylococci species or other gram-positive bacteria. The femA nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the femA nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections.
Sequence 1371 BP; 545 A; 155 C; 248 G; 423 T; 0 other;
Query Match 48.8%; Score 626; DB 20; Length 1371;
Best Local Similarity 69.0%; Pred. No. 5.3e-103;
Matches 887; Conservative 0; Mismatches 395; Indels 4; Gaps 2;
Qy 2 cactggaattgaagctttacaaataaaatgcgcgtacgcgattttcacacaagcagtag 61
Db 86 caaagagattcggcgattcagcgaataaaatgcgcgaatgattttacgcaaatggtg 145
Qy 62 gtaattatgaattaaacacatctgaagtgacttcaacacacatttagtaggggtcaagata 121
Db 146 gaaattatgaattaaatgcgaagtagacagaacacacatttagtaggtattagaata 205
Qy 122 atcaagtggaattatagctgcgtctgttaacaagtgaccagttatgaagaattta 181
Db 206 atgataatgaagtaattgcgcgtgttactcacagctgttctgtttagaaattctca 265
Qy 182 attactttactcaaatagagccagtgattgattgacacaaagaactgtgtgact 241
Db 266 agtatttttcccaatagaggccagtcagtagattttgaaataaagaactcgtacatt 325
Qy 242 tttctttaaagaatcgtgagctattttaaagttataaaggattttcttagaatcg 301
Db 326 acttcttaacgaattagcaaaatgatgaaaaacataatgcgccttatacttccagtag 385
Qy 302 atccttacttgccatatacctaagaagatcatggtgcaatattataaaatcattcaacc 361
Db 386 atccttactgtctcataatcgttaactcagtggtggaagtattagcaaatgcgggtc 445
Qy 362 gtgattgttaataaacaatttgaatcattaggtttatgaacacacaggggttcacactg 421
Db 446 acgatttgattttgataaaatgaacaactcgtttataagcagtgaggttttttaactg 505
Qy 422 gtttccaccacatacacaatagatggcggttctgtactgtattgaaagatggaagc 481
Db 506 gctttgacccaatacttcaataaagattccattctgttttagatttagctgggaaactg 565
Qy 482 aaagagcgtcatcaagaacatggacagtttaagaaaagaataactaaagaatttcaaa 541
Db 566 ctaaagacgtacttaattggttaggtttacgttaacgcgaataactaaagaatcaga 625
Qy 542 aaaaatggtttaaagtcgtttttcttactaaagatgaatgcccgtatttccgtcaattta 601

626 aaaaatggtttgaaagtaagatttttaggtgaagtaggttgcgaattattccgtcattca 685
Qy 602 tggagatactacagagaagaagattttcaacacgactggtgcgagactttctatacaata 661
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Qy 662 gattaaaatcctttgaaaa---tgtaagaattccttttagcatatataagactttgaaact 718
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Qy 779 agatttgaagaagaacagataatacaaaaacgattataataaaatagacaacttaaac 838
Db 866 agtatatgaaaaagaccagaataaaataaaagcgtataataaaaaaagaatttagaac 925
Qy 839 aacaaagagaagcaaatgaagcttaaatagaaagcacttcaactacacacaagaacatg 898
Db 926 acaactgattgcaaacacaaacaaataagatgaagccactggttacaagaagacatg 985
Qy 899 gtgatacatattccaaatgacgcgtggtttctttattattatttaacattggaagtgtatt 958
Db 986 gtaacgaattacccgatttctgcagcttactttattattatttcccttgaagcgtttact 1045
Qy 959 atcagtggttgcatacgaatgaatcgtcacttgcagtgtagttgcaattcagtgagg 1018
Db 1046 atcgagtggtacatctaatgaattagacatttgcgtggtggttagtgaatacaatgga 1105
Qy 1019 aaatgattaaatcagcgttagatcaacaacattgacccgttataactcttctgtgtacagc 1078
Db 1106 agatgattcaattcattctatagataataatagatagataataattttttagttattg 1165
Qy 1079 gagacttccagaagatgcacctgagtggttgcgttattataattttaaagagttacaatg 1138
Db 1166 gtcattttactgaagatgcagaagatgcaggtgttgcgttataattttaaagaggtttta 1225
Qy 1139 cagatgtttatgaatatattgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1198
Db 1226 cagatgttagtaaatgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 1285
Qy 1199 catatacaacact-aaaaaaagattataaaaaataaaataaagattttcagtaagaggaatt 1257
Db 1286 tttatagacattgaaaaaaatgaagataaaaaaagaataaataaataaagaagggaact 1345
Qy 1258 tagataatgaaatttacagagttta 1283
Db 1346 aagctagaatgaaatttacagagttta 1371
RESULT 3
AA337804
ID AAX37804 standard; DNA; 1342 BP.
XX AAX37804;
AC AAX37804;
XX 09-JUL-1999 (first entry)
DT XX
DE XX
DE Staphylococcus hominis FemA DNA.
XX FemA; identification; detection; therapy; infection; femB;
XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX Staphylococcus hominis.
OS Location/Qualifiers
XX Key 64..1327
XX CDS /*tag= a
XX /product= "femA"
XX
XX W09916780-A2.

XX This invention describes novel *Staphylococcus*-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown *Staphylococci* species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different *Staphylococci* species or other gram-positive bacteria
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against *Staphylococci* infections.

Query Match	48.18;	Score 617.6;	DB 20;	Length 1342;
Best Local Similarity	70.0%;	Pred. No. 1.7e-101;		
Matches 860; Conservative	0;	Mismatches 364;	Indels 4;	Gaps 2

[illegible]

[illegible]

ID AAX37798 standard; DNA; 1305 BP.
 AAX37798;
 AC 09-JUL-1999 (first entry)
 DT
 XX Staphylococcus haemolyticus FemA DNA.
 DE
 XX FemA; identification; detection; therapy; infection; femB;
 KM amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX Staphylococcus haemolyticus.
 OS
 XX Key Location/Qualifiers
 FT CDS 4..1305
 FT /tag= a
 FT /product= "FemA"
 XX
 XX MO9916780-A2.
 XX
 XX 08-APR-1999.
 XX
 XX 28-SEP-1998; 98MO-BE00141.
 XX
 XX 26-SEP-1997; 97EP-0870146.
 XX
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (U10-) UNIV CATHOLIQUE LOUVAIN.
 XX
 XX Gala J, Vannuffel P;
 PI
 XX
 DR MPI: 1999-287521/24.
 DR P-FSDB; AAY08215.
 XX
 XX New Staphylococcus-specific oligonucleotides
 PS Claim 15; Fig 6a-b; 48bp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 CC
 XX Sequence 1305 BP; 513 A; 165 C; 222 G; 405 T; 0 other;
 SQ
 Query Match 46.3%; Score 594.2; DB 20; Length 1305;
 Best Local Similarity 67.7%; Pred. No. 2.5e-97;
 Matches 867; Conservative 0; Mismatches 403; Indels 11; Gaps 2;

Db 211 tttattctaacgcagaccgttaattgattatgataatagagagctgttccttttc 270
 Qy 247 ttttaagaatctgtgagcatttaaaagtataaagattattctttaagaatcgtctc 306
 Db 271 tttatgtatgaacaaagatttaaacagcataattgtctatagttcgagttgacct 330
 Qy 307 tacttgccatcatcaactaagaagatcatgtgcaatalttaaaaatcatcaacctgtat 366
 Db 331 tattaccatcatcaatttaattcaatgtgtgaattacagtaatgctgtaagat 390
 Qy 367 ggtttaataacaatttgaatcatgtatgtatgaacaccagagcttcacactgtgttc 426
 Db 391 tggttcttggataagatgaagcatctcgatcttgaacaaggaaggtttactcaaggttt 450
 Qy 427 cccccaatacgaataattagatgagcatctgtactgtattgaagaagatgagcgaaga 486
 Db 451 gatccgattaaacaatccgatacatctctgttttagatttaaaaaataacaatcaaa 510
 Qy 487 acgctcatcaagaacatgagcaggtttaagaagaatactcaaaaagttcaaaaat 546
 Db 511 gatataatnaatgtgaatgagatgactgatacgtataactcaaaaagttcaaaaat 570
 Qy 547 ggtgttaagttcgtttctatcttaagaatgaatgacgataatccgataattatgaa 606
 Db 571 ggtgttaagttcgtttctatcttaagaatgaatgacgataatccgataattatgaa 630
 Qy 607 gatatacagaggaagaagattcaacagctgtgagatcttcatatcaaatagatta 666
 Db 631 gatatacagaggaagaagattcaacagctgtgagatcttcatatcaaatagatta 690
 Qy 667 aatattctgaat--gtaaagattcccttaagcatatataactttgaacttaata 723
 Db 691 agacatttcaagatcagcagctgtgactgatacagatgattatgaattgtatgatactc 750
 Qy 724 ccacattagaanaagacatgatacaatacaagaatattgcaaaagctgaanaagat 783
 Db 751 gaagaatttcaaaatgaaacgtgaaacttcaataaagatgttaataagctttaaagat 810
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 Qy 904 acattaccatgagcgtgtgttcttattatcaatcatcttgaagttgataatgca 963
 Db 931 gaattaccaatttcaagagtttcttattatcaatcatcttgaagttgataatgca 990
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 Qy 1024 attaatacgcgttatgatacacaacttgcagcgttaacttcatgtatgcaggaac 1083
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 Qy 1084 tctctagaagttgacactgtgttgcgttataaatttaaaaaagttacaaatgcagat 1143
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 Qy 1144 gttctgataatattgtgatttcgttaaaccaatataaaccgcgtataacagcat 1203
 Db 1171 gtaattgtatgttggagacttgcgttaaaccttaaacacacttgcgtatgcgtat 1230
 Qy 1204 acacaacataaaaagratataaaaataatgatttcgtgaaggaaggaattatgata 1263
 Db 1231 aagacacataaaaagratataaaaataatgatttcgtgaaggaaggaattatgata 1282
 Qy 1264 atatgaattttagagattaa 1284

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Db	2894	gaatttaagacttlaacgtaatcgtaatgaacataatgatacttataacaaatggaaagtgat	2953
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Db	2954	taagaatttaaaagtgctgcgaagtagccaggtacacatttagttggaatttaaaatagat	3013
Oy	127	ggtvgaattatagctgcggtctgtttaacaagtgtaaccggtatagaagaatttaattac	186
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Oy	187	ttttactaaatagaggaacgaatagattatgaacaaacaaagaactgttgacttttc	246
Db	3074	ttttattccaacgcgggtccagtaattagattataataataaagagctgtgacatttttc	3133
Oy	247	tttaagaagaatcgtgagactatttaaaagttataaagattcttttagaactcgcttc	306
Db	3134	tttaatgatttgaaataatgtaaaaaaataattgtttattttaaggttgaccoca	3193
Oy	307	tactgtccatccaactcaagagtgatggtgcgaatttaaaaaatcattcaacgcgtat	366
Db	3194	tacctccaatacattatttaaatacgtgggagaaataactcgsaaatgcgcgtatg	3253
Oy	367	ggttatttaaacatttgatcatattagattatgaacacacgaagcttcaactggttc	426
Db	3254	tgaatttttggaaattagagaggtttagatataaacaagaaggtccacaagaagatt	3313
Oy	427	caccaatacacaataatagatgagctctgtactgtatttagaagtatgscgaaag	486
Db	3314	gattcgttatccaataccgtatcatctgtcttcaatttttagcaaaaaaagtgtaat	3373
Oy	487	acgctcaagaacatgagacggtttaaaaaaagaataactcaaaaaagttcaaaaaat	546
Db	3374	gactttttaaanaacatggaatggttttaagaagcgtaactcaaaaagttaaagaaat	3433
Oy	547	gggtttaagttggtttctctactaaagtgtaatgcccgaattccgtcaatttaagaa	606
Db	3434	ggagtttaagatccgcttttctcgtgaagaaggttacctataattgagtcatttaag	3493
Oy	607	gatactacagagaagaagaattccaagatcggtgagatgacttattacaatagat	666
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Oy	667	aaatactttgaaaa--gttaagattcccttagacataatagactttgaaacttaact	723
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Db	3794	gaattaccatctcgtgctcttcttataattacgcgtttgaaagtattactaagct	3853
Oy	964	ggtgtgtacatgaatgatatcgtcaactttgcaggtatgataacatcagttggaag	10233
Db	3854	ggtvgactccaactcgtttatcgcatttttgcaagggcatacggtttcaatgaaag	39133
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Page 12

QY 58 gtagtaattatgataaaacatctgaaggtacttcaacacatttagtgaggcca 117
| | | | | | | | | | | | | | | | | |
Db 4 gaagtaattcagaattaangttgcgaagtaccgagtcacaatttagttgaa 63

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OY	178	ttaataattcttaacttaaatatgagagcccggtatagattatgacgaacaaagaacttgt	237
Db	124	ttaataattcttatttccatctgcggtcccgtaaatgattataataataaagaagctgtga	183
OY	238	gaattttctttaagaanaacgtgtgacatttaanaagttaaagttaaagaattatcttga	297
Db	184	catttttctttaaataatgtatggtaataatgtlaanaaataataattgtttatttaaga	243
OY	298	atcgatccttaactgtgcataatcaactaagaatcatatgatatggaatgttaanaaatcatcc	357
Db	244	gttgaccataacttcatactatatttaataatcatatgagtggaataactgtgaatgtga	303
OY	358	aaccgtgatgtttcaatttaacaatttgaatcatcatagttatgaaacacaaaggtctaca	417
Db	304	gttccatgttgattctttcttgtaattagaaggttttagataataacacgaaggttccac	363
OY	418	acgtgttccaccacaatacatcaactatagatgtgcattctgtactgtatttgaagtatg	477
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OY	478	gacgaanaagacgtcatcaagaacatgtgacagtttaagaaanaagaaatcacaaanaagtt	537
Db	424	agttcattatgattgtttaanaaacaatgtgttttaagaagaacgttaatacctaanaagtt	483
OY	538	caaaaaatcgtgttaaatgttcgttttccatctaaagaatgaataatgcgatalccgtcaa	597
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OY	598	ttttgtgaagaattacacagaagaagaagatttcaacgattcgtgtgcgtgacttctattac	657
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OY	658	aatagattaataactttgaaa---tgtaagattctctttagcatataagacttgaa	714
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OY	715	acttaattccaaatttgaaanaagaacatgacaatatacaacaagaatatgtcaaaagct	774
Db	664	gagttataagagaatcaataataatgaagaagaatgtgttaataagattataataagct	723
OY	775	gaaaagaatttgaanaagaaacacgaatatacaaaaaogattataataatgaacaacta	834
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Db	784	gaacaacaactcgtatgcataatgaacanaaataatgaagacttaanaacttaaaacaaga	843
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Db	844	catgtcaatgtatcacocctctcgtcgtcttcttataataatccgttttgaagtgt	903
OY	955	tattatgcaagttgttcatacgataatgaatatcgtccactttgcagtgagtattgaattcag	1014
Db	904	tactaagctgtgtgaacttcaaatcgttatcgtcatcttgcagggagactatggtgtcaa	963
OY	1015	tgggaaatgtattaatcoggtttagatcaacaactgtacacgttaacttctatgtatc	1074
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OY	1195	aaagcatatacaacacttaaaaaaagatttaaaaa	1229

QY	7	gaattgaagctttacaaataaaacgcgcgtacgcattttacacagcagctaggtaat	bo
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QY	67	tatgaattaaaaacatctgaagtgacttcaacacatttagtggggtcaagagataacaa	126
Db	104	tanganntnaannttgcnannnnnnnganncncanntagtngnataaanaanaant	163
QY	127	ggtagagattagctgcgtctgtctaaacaagtgaccagttatgagaataattcaattac	186
			223

Page 14

Db 4077 ctcatcacacaatctgtctcatcttgaatatagaataaccatcagaalaaatgcgc 413

QY	101	attttagtgggttcacagaataacgaagttgaatltagtcgtgtctcgttaacaatg	160
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QY	161	taccagttatgaagaattaatcttactttaccgaatgagcgagtaatgagtttg	220
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Db	4317	acgcttatatgttttaactgaccccttccgcttgagaataattcgaaagttgagagag	4376
QY	341	atatataaatacatcaaccggatgggtttaataacattgaacattgaactagtattg	400
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Db	4497	taaacctagaataataagatganaaacaattgttaanaagaatggattatcaacaacgcc	4556
QY	521	gaactactaaaagtctaaanaaatggtgttaagttctgttctctactcaaatgtaa	580
Db	4557	gtaatattagaanaacctaigaatgcaggtgaaagtcgcgattatcaaatatgaa	4616
QY	581	tgcagatattcgcataattgtagaagatfacacagagaagaatctcaacgatctg	640
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QY	641	ggcattgactctattacaatgat---taaatactttgaaatgtgaaagttccttag	697
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QY	698	catatataagctttgaactatccattccacaattgaaanaagaacatgacaatatcaaa	757
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QY	1178	ttaataaacgcgtacaaagcatatatacaacctaataaaagatttaaaa	1228

infection by *Staphylococcus*. The isolated nucleic acid molecules are also useful for generating probes and primers, and in the recombinant production of femX protein.

xx Sequence 1470 BP; 604 A; 146 C; 237 G; 483 T; 0 other

Query Match	25.1%	Score 322.4;	DB 20;	Length 1470;
Best Local Similarity	54.0%	Pred. No. 7,3e+4;		
Matches 681;	Conservative	0;	Mismatches 576;	Indels 3;
				Gaps 1

[illegible]

us-09-509-234c-50.rng

Fri Jun 21 08:38:26 2002

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Db 1289 ttgggtgtcaacaatttaaaagggttttaatgcacatgttgaagaattattggtgat 1348
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Db 1349 ttcatcaaacccagtaagaccattctatatataaaattgcataactttataaggttttaa 1408
QY 1225 aaaaaataaatgatcttcagtaagaggggaatttagataatataatgaaatttacagagtttaa 1284
Db 1409 ttataagtgatgttggaaattgaaatttttaattctttccacaacatctttcacttttta 1468

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Search completed: June 20, 2002, 14:46:55
Job time: 18805 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 12:04:07 ; Search time 208.59 seconds
(without alignments)
1512.026 Million cell updates/sec

Title: US-09-509-234C-50
Perfect score: 1284
Sequence: 1 acactgaattgaagcttt.....taagaaattacagagttaa 1284

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match		Length	DB ID	Description
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1	574.4	44.7	1257	1	US-08-330-154-1	Sequence 1, Appli
2	216.2	16.8	453	3	US-08-714-918-9	Sequence 9, Appli
3	216.2	16.8	453	4	US-09-265-315-9	Sequence 9, Appli
4	216.2	16.8	453	4	US-09-265-315-9	Sequence 9, Appli
5	216.2	16.8	453	4	US-09-266-417-9	Sequence 9, Appli
6	194	15.1	410	3	US-08-714-918-6	Sequence 6, Appli
7	194	15.1	410	4	US-09-265-315-6	Sequence 6, Appli
8	194	15.1	410	4	US-09-266-417-6	Sequence 6, Appli
9	194	15.1	410	4	US-08-714-918-4	Sequence 4, Appli
10	139.6	10.9	400	3	US-08-714-918-4	Sequence 4, Appli
11	139.6	10.9	400	4	US-09-265-315-4	Sequence 4, Appli
12	139.6	10.9	400	4	US-09-266-417-4	Sequence 4, Appli
13	139.6	10.9	400	4	US-09-266-417-4	Sequence 4, Appli
14	83.8	6.5	5253	3	US-08-714-918-19	Sequence 19, Appli
15	83.8	6.5	5253	4	US-09-265-315-19	Sequence 19, Appli
16	83.8	6.5	5253	4	US-09-265-315-19	Sequence 19, Appli
17	83.8	6.5	5253	4	US-09-266-417-19	Sequence 19, Appli
18	69	5.4	240	1	US-08-628-417-6	Sequence 6, Appli
19	66.8	5.2	2223	1	US-08-257-073-4	Sequence 4, Appli
20	66.2	5.2	7218	1	US-08-232-463-14	Sequence 14, Appli
21	61.8	4.8	658	4	US-08-998-416-595	Sequence 595, App
22	60.6	4.7	2447	2	US-09-014-969-14	Sequence 14, Appli
23	60.4	4.7	930	4	US-08-936-165A-74	Sequence 74, Appli
24	59.6	4.6	19124	2	US-08-487-826B-13	Sequence 13, Appli
25	57	4.4	6243	4	US-09-056-075-1	Sequence 1, Appli
26	55.8	4.3	1956	4	US-08-559-896B-1	Sequence 1, Appli
27	55.2	4.3	2674	4	US-09-817-180-1	Sequence 1, Appli

c 28	55.2	4.3	6243	2	US-09-056-075-1	Sequence 1, Appli
c 29	53.4	4.2	1798	4	US-09-797-906-1	Sequence 1, Appli
c 30	52.8	4.1	1021	3	US-08-714-918-70	Sequence 70, Appli
c 31	52.8	4.1	1021	4	US-09-265-315-70	Sequence 70, Appli
c 32	52.8	4.1	1021	4	US-09-265-315-70	Sequence 70, Appli
c 33	52.8	4.1	1021	4	US-09-266-417-70	Sequence 70, Appli
c 34	52.8	4.1	1021	4	US-07-867-106-2	Sequence 2, Appli
c 35	52	4.0	6152	4	US-08-973-462-1	Sequence 1, Appli
c 36	51.4	4.0	6671	1	US-08-280-443-1	Sequence 1, Appli
c 37	51.4	4.0	6671	1	US-08-457-459-1	Sequence 1, Appli
c 38	51.4	4.0	6671	1	US-08-555-678-1	Sequence 1, Appli
c 39	51.4	4.0	6671	5	PCT-US95-02275-1	Sequence 1, Appli
c 40	51	4.0	6124	4	US-08-213-419B-3	Sequence 3, Appli
c 41	50.8	4.0	1051	4	US-09-245-041-10	Sequence 10, Appli
c 42	50.4	3.9	1891	4	US-08-973-462-3	Sequence 3, Appli
c 43	49.8	3.9	1320	1	US-08-257-073-15	Sequence 15, Appli
c 44	49.8	3.9	1482	4	US-08-038-327E-41	Sequence 41, Appli
c 45	49.8	3.9	1482	4	US-08-098-327E-45	Sequence 45, Appli

ALIGNMENTS

RESULT 1
US-08-330-154-1
; Sequence 1, Application US/08330154
; Patent No. 5587307
; GENERAL INFORMATION:
; APPLICANT: Alborn Jr., William E
; APPLICANT: Hoskins, Joann
; APPLICANT: Skatrud, Paul L
; APPLICANT: Unal, Serhat
; TITLE OF INVENTION: FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
; TITLE OF INVENTION: FEMA PROTEIN, AND VECTORS AND MICROORGANISMS COMPRISING
; TITLE OF INVENTION: THE FEMA GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Division/AEH
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,154
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,925
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US/08/057,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamilton, Amy E
; REGISTRATION NUMBER: 33,894
; REFERENCE/DOCKET NUMBER: X-8894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3169
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS


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?      FILING DATE: September 13, 1996
?      APPLICATION NUMBER: 60/009,102
?      FILING DATE: December 22, 1995
?      APPLICATION NUMBER: 60/003,798
?      FILING DATE: September 15, 1995
?      ATTORNEY/AGENT INFORMATION:
?      NAME: Warburg, Richard J.
?      REGISTRATION NUMBER: 32,327
?      REFERENCE/DOCKET NUMBER: *240/247
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (213) 489-1500
?      TELEFAX: (213) 955-0440
?      TELEX: 67-3510
?      INFORMATION FOR SEQ ID NO: 9:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 453 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      PS-09-265-315-9

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Best Local Similarity	66.2%;	Pred. No. 2.6e-39;		
Matches 296;	Conservative 0;	Mismatches 151;	Indels 0;	Gaps 0;

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Qy	906	attaccaatagcagctgggttcctttattataatccattgaagttgatatattatcgagg	965
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RESULT      4
US-09-265-315-9
: Sequence 9, Application US/09265315
: Patent No. 6187541
: GENERAL INFORMATION:
: APPLICANT: Benton, Bret
: APPLICANT: Lee, Ving J.
: APPLICANT: Malouin, Francois
: APPLICANT: Martin, Patrick K.
: APPLICANT: Schmid, Molly B.
: APPLICANT: Sun, Dongxu
: TITLE OF INVENTION: METHODS OF
: TITLE OF INVENTION: ACTIVE ON S
: TITLE OF INVENTION: TARGET GEN

```

[illegible]

RESULT 3
 US-09-265-315-9
 Sequence 9, Application US/09265315
 Patent No. 6187541
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match	16.8%	Score 216.2	DB 4	Length 453
Best local Similarity	66.2%	Pred. No. 2.6e-39		
Matches 296	Conservative	0	Mismatches 151	Indels 0
QY	666	aaataactttggaataatgtaaaagatcttcctctagcatatataagactttggaacttacatcc	725	
Db	7	ATATTTCMAAGACCGTGTGTAGTACTTTCAGCGTATTCACACTTAAATGAAATATATPA	66	
QY	726	acatttgaanaaagaacatgagacaatacaacaanaagatatgcaaaagcttgaanaagatt	785	
Db	67	AGAACTTAACGAGAGACGTGATTTTAAATTAAGATTAAATTAAGCTTAAGATAT	126	
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Db	127	TGAAAAAGCTCTGAAATTAATAAAGCAGCATCAAGCGAGTAACTTTCACACAACT	186	
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Db	187	TGATGCAATGAGCAAAAGTGAAGACGGTAAAGCTTCAGAGANCAATGATATGN	246	
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Db	247	TTTAACTATCTCTCTGTTTCTTCTTTATCAATCCNTTANNTGGTTTATATAGCTGG	306	
QY	966	tgttcatgaaatgaatcatcgcacacttgcaggtagtagtaagaacttcagtgggaaatgat	1025	
Db	307	TGGACATCAAAATGCTNTCCGTATTTTTCGGAGNATATGCTACGTGGAATGAAATGNT	366	
QY	1026	taaatcagcgttagatcacacaacattgacgcgttatataactctatggtatcagggagactt	1085	

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D_b 427 TNCAGNAGTGCTGTAGAGATGCTGGTGT 453

RESULT 5
 US-09-266-417-9
 Sequence 9, Application US/09266417
 Patent No. 6228588
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Viny J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongyu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/266,417
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,796
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/248
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-266-417-9

	Query Match	16.8%;	Score 216.2;	DB 4;	Length 453;
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	Matches 296; Conservative	0;	Mismatches 151;	Indels 0;	Gaps 0;
Qy	666 aaatccttgaagaattgaagttccotttcgttatagactttaacattcacctc	725			
	I I				
Dd	7 ATATTACAAGACCGCTGTGTTACTTCCTTTAGCCTATATCAACTTTAATAATATTTAA	66			
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APPLICATION NUMBER: US/09/203,313

Fri Jun 21 08:38:26 2002

us-09-509-234c-50.rn1

Page 6

FILED DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-6

Query Match 15.1%; Score 194; DB 4; Length 410;
Best Local Similarity 68.2%; Pred. No. 2e-34;
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695 tagcatatagacttgaacttccatcaccataggaaagaacatgaacataca 754
61 TAGCGTATATCACTTAATTAATTAATTAAGACTTAACAAAGACCGTGTGTAAGTCTT 120
755 acaagatattgcaaaagctgaaagaattagaagaacacagatacaaaacga 814
121 ATAAAGATTAAATTAAGCTTAAGGATTTGAAGAAACGCTGTAATTAAGAAACGAC 180
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181 ATAAAGAGGAGATTAATTAATTAAGCAACATTTGCAAAATGAGCAAAAGATTGAAGAG 240
875 cacttcaactcaacaagaacatggtgatacattaccatagacgtggttcttatta 934
241 GTAACGCTTCAAGAGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
935 ttaacatattgaattgataattatgacagtggttcaatgaatgaatgccttga 994
301 TCAATCATTGAGTTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
995 caggtgattgacatcagtggaagaatgataataatgaacgttgaagta 1043
361 CCGGAGATTATGCAAGTGAAGGAAATGATTAAATTAATTAATTAATTAATTAATTAATTA 409
RESULT 8
US-09-265-315-6
Sequence 6, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-6

Query Match 15.1%; Score 194; DB 4; Length 410;
Best Local Similarity 68.2%; Pred. No. 2e-34;
Matches 279; Conservative 0; Mismatches 127; Indels 3; Gaps 1;
638 gtggcgatgctctcttaccatagatgaataacttgaaga---tgaagattcctt 694
1 GTAATGCAAAATTAATTAAGCTTAACCTTAATTAATTAACAAAGACCGTGTGTAAGTCTT 60
695 tagcatatagacttgaacttccatcaccataggaaagaacatgaacataca 754
61 TAGCGTATATCACTTAATTAATTAATTAAGACTTAACAAAGACCGTGTGTAAGTCTT 120
755 acaagatattgcaaaagctgaaagaattagaagaacacagatacaaaacga 814
121 ATAAAGATTAAATTAAGCTTAAGGATTTGAAGAAACGCTGTAATTAAGAAACGAC 180
815 ttaataaatgacacacttaaaacaaagaagaacatgaagtaagtaagaaga 874
181 ATAAAGAGGAGATTAATTAATTAAGCAACATTTGCAAAATGAGCAAAAGATTGAAGAG 240
875 cacttcaactcaacaagaacatggtgatacattaccatagacgtggttcttatta 934
241 GTAACGCTTCAAGAGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
935 ttaacatattgaattgataattatgacagtggttcaatgaatgaatgccttga 994
301 TCAATCATTGAGTTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
995 caggtgattgacatcagtggaagaatgataataatgaacgttgaagta 1043
361 CCGGAGATTATGCAAGTGAAGGAAATGATTAAATTAATTAATTAATTAATTAATTAATTA 409

Db 361 CCGAAGTTATGTCAGTGAATGGGAATGATTAAATTCATTAATCA 409

RESULT 9

US-09-266-417-6

; Sequence 6, Application US/09266417

; Patent No. 6228588

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/266,417

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 240/248

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 410 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-266-417-6

Query Match 15.1%; Score 194; DB 4; Length 410;

Best Local Similarity 68.2%; Pred. No. 2e-34;

Matches 279; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

Qy 638 gtggcagatctctattacataagattacattcttgaataaattcttccctt 694

Db 1 GTATGACAAATNTAACTACGCTTAAATATTACAAAGCCGTGTGNAGTACCTT 60

Qy 695 tagcatatagattgaaattacattccacaaattagaaaaaacatgaacaataca 754

Db 61 TAGCGTATATCAACTTAAATGAATATTAAGAAGCTAAACGAGAGCGTATTTTAA 120

Qy 755 acaaaatattcgaac 814

Db 121 ATAAAGATTAAATTAAGCGTTAAAGGATATTGAAAAACGCTCTGAAAAATAAAAGCAC 180

Qy 815 ttaataaataagacaacttaaaacaaagaagaagaacaaatgaagctaaattagaagaag 874

Db 181 ATAACAAGCGAGATAACTTTACAACAACACTTGTATGCAAAATGAGCAAAAGATTGAAGAAG 240

Qy 875 cacttcaactacaacaagaacatggatgatacattaccataagcagctgggtcttttatta 934

Db 241 GTAAACGCTACAAGANGAACATGGTAATGAATTAACCTATCTCTNCCTGGTTCTNCTTTA 300

Qy 935 ttaatccattgaagtgtattatgcaggggtggttcacgaatgaatgcacgttcacgttg 994

Db 301 TCAATCCATTGANGTTGTTTATTATGCTGGTGTACATCAATGCAATCCGTCATTFTTN 360

Qy 995 caggtagttatcgaattcagtggaagaatgattaaatacgccttagatca 1043

Db 361 CCGAAGTTATGTCAGTGAATGGGAATGATTAAATTCATTAATCA 409

RESULT 10

US-08-714-918-4/c

; Sequence 4, Application US/08714918

; Patent No. 6037123

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,918

; FILING DATE: September 13, 1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 222/005

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 400 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-714-918-4

Query Match	10.94;	Score 139.6;	DB 4;	Length 400;
Best Local Similarity	60.04;	Pred. No. 1.9e-24;		
Matches 240;	Conservative 0;	Mismatches 159;	Indels 1;	Gaps 1

STREET: Suite 4700
CITY: Los Angeles
STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-4

Query Match 10.9%; Score 139.6; DB 4; Length 400;
Best Local Similarity 60.0%; Pred. No. 1.9e-22;
Matches 240; Conservative 0; Mismatches 159; Indels 1; Gaps 1;
Qy 202 ggaccagtaaggattatgacacaaagaactgttgacttttttttttaaaagaatcgtg 261
Db 400 GGTCCAGTGATTGATGAAATCAAGNACTCGTACACTTTTNCCTTAATGAATATCC 341
Qy 262 agc-tattataaagattatgacacaaagaactgttgacttttttttttaaaagaatcgtg 320
Db 340 AAAATATGTTAAATAAATCAAGNACTCGTACACTTTTNCCTTAATGAATATCC 281
Qy 321 actaagagatcattgacacaaagaactgttgacttttttttttaaaagaatcgtg 380
Db 280 ATACTGATCATGATGCGGAGATTACAGTAAATGCTGTAATGATGGTCTTTGATAA 221
Qy 381 attgaatcattgacacaaagaactgttgacttttttttttaaaagaatcgtg 440
Db 160 AATCCGTTATCACTAGTGTAGATTTAAAGTAACAGCAGATGACATCATTAATAA 101
Qy 441 aattagatggcattgacacaaagaactgttgacttttttttttaaaagaatcgtg 500
Db 501 catgacagtttaaaagaactgttgacttttttttttaaaagaatcgtg 560
Db 100 TATGATGCGACTTGAAGAAAGAACACGGAANNAGTTNAAAGAAAGATGCTGTTAAAGTAAG 41
Qy 561 ttctctctaaagatgaatgcgatatttcgcgaattt 600
Db 40 ATTTTATCTGAGGAGNACTACCAATTTTATGATTATT 1

RESULT 13
US-09-266-417-4/c
; Sequence 4, Application US/09266417
; Patent No. 6228588
; GENERAL INFORMATION

APPLICANT: Benton, Bret
APPLICANT: Lee, Vang J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-4

Query Match 10.9%; Score 139.6; DB 4; Length 400;
Best Local Similarity 60.0%; Pred. No. 1.9e-22;
Matches 240; Conservative 0; Mismatches 159; Indels 1; Gaps 1;
Qy 202 ggaccagtaaggattatgacacaaagaactgttgacttttttttttaaaagaatcgtg 261
Db 400 GGTCCAGTGATTGATGAAATCAAGNACTCGTACACTTTTNCCTTAATGAATATCC 341
Qy 262 agc-tattataaagattatgacacaaagaactgttgacttttttttttaaaagaatcgtg 320
Db 340 AAAATATGTTAAATAAATCAAGNACTCGTACACTTTTNCCTTAATGAATATCC 281
Qy 321 actaagagatcattgacacaaagaactgttgacttttttttttaaaagaatcgtg 380
Db 280 ATACTGATCATGATGCGGAGATTACAGTAAATGCTGTAATGATGGTCTTTGATAA 221
Qy 381 attgaatcattgacacaaagaactgttgacttttttttttaaaagaatcgtg 440
Db 220 AATGAGTAACCTTAGGATTTGAACATACACTGATTTCCATTAAGGATTTGATCTGCTGCTACA 161
Qy 441 aattagatggcattgacacaaagaactgttgacttttttttttaaaagaatcgtg 500

Page 10

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Query Match      6.5%; Score 83.8; DB 3; Length 5253;
Best Local Similarity 44.5%; Pred. No. 7.3e-10;
Matches 389; Conservative 1; Mismatches 473; Indels 12; Gaps 1

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Qy	437	atcaaatatgacgcatcttcgctactctgattagaagaattgacgaagaagcctcatca	496
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Qy	497	agacatgacgcagatttlaagaaaagaactaataaaagtlcaaaaaatgtygttaag	556
Db	2843	ATAGTTTGAACGCCGAATGCTTCAAAAGTGCCCTGGCTTTAAAGCGGATGACGACG	2784
Qy	557	ttcgltttctatcaatgaatgaatgacgcatcttcgltcaattttatggaagatcacag	616
Db	2783	TGAGACGATGCTGATGAGACAGATTTAAAAACCTTTGCTGATGATTAATGAAAATACTCGGG	2724
Qy	617	agaagaagaagttcaacagatcggttgagagactctatcaatcatagatlaaaatctg	676
Db	2723	AACGGGATGGCTTTAAACGGGTATATTAGTTACTTTGAAAATTTATATGATGCGTTGC	2664
Qy	677	aaaatgtaaaagatcccttttagcabatataagacttgaacctatcatcccaatgaagaa	736
Db	2663	ATGAGATGAGCGATGCTGACATTTATTTTGTAAAGTTGATCCAAAGAAAATATAGCGA	2604
Qy	737	aagaacaatgacaatacaacaagaatattgcaagaagcgtgaagaagattagaaga---	793
Db	2603	AAGTAAATCAAGATTTGAATGACCTTATGCCGAATTTGCTAAATGGCAGCAGAAATGA	2544
Qy	794	-----aaccaagataacaaaaacgattaaataatagaacaacttaaacaca	844
Db	2543	AAMACTCTGAAAAACAGATGATAAAAACCGAAATATGATTAATGATGCGCAAAATATAA	2484
Qy	845	gagaagaacaatgaaagctaaattagaagaagcactcaactcaacaagaagaatgagata	904
Db	2483	TTGCTTAAATTAAGATTTTAAACGACACCTGAGAGCTTTGAAAAAGGACATCTGTAAG	2424
Qy	905	catcaacaatgagcgttggttcttcttaatacatccattggaagtgtatattagcag	964
Db	2423	GTATTTATCTTTCTGGTGACATTAATTAATGTTTGGTGGCTCAAAATCATTAATTATATG	2364
Qy	965	gtgtgtcatcgaatgaatatacgtcaactgtgcaggtagttatgcaattcagtggaatga	1024
Db	2363	GTGCGCTCTCTAATGAAATTTAAGATTTTAAACCAATCATATATGCAATGATACGTGA	2304
Qy	1025	ttaataagcggttgcatacacaacatgcagcogtttaactcttaagttatcagcggagact	1084
Db	2303	TGAAGTATCCACGTGAACATAGTGTCAACACTTTGCAATTTGCGTGTACAGATAATATC	2244
Qy	1085	tcccaagaatgcacccgatgtytgcgcttataaatttaaaaaagtgtaacatgcagatg	1144
Db	2243	CAGTATAAATCAGAACATTTATGATTAATGGCATTTTAAAAAGTGTTGGGACAAATACT	2184
Qy	1145	ttatagataattgtgtgatttcogtttaaccaattataaacaacggttcaagaagata	1204
Db	2183	TAACTGAAAAAGATTGGCAATTTGATATGATTAATGATGCAATTTGTACCAATTAATG	2124
Qy	1205	caacactaaaaaagttcttaaaaaataaagatt 1239	
Db	2123	AGCAAGTTAAACCGGTTTAAACAAAAGCTAAATTT 2089	

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RESULT 15
US-09-265-315-19/c
Sequence 19 Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vling J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 671-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-19

Query Match 6.5%; Score 83.8; DB 4; Length 5253;
Best Local Similarity 44.5%; Pred. No. 7.3e-10;
Matches 389; Conservative 1; Mismatches 473; Indels 12; Gaps 1;

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DB   2963  AAAATTTGAAAGCGCTGGTGTTAACCAATAAAGANTTTAAAGAAGTTTATCAAAGACT 2904  
  
QY   437  atcaaattagatggcttctgacttgatttagaaagtgcacaaaaagcgctcatca 496  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
DB   2903  ACATCCAACCAGTATGACTATGATTACCACAATTGATAAAAATGATGATGAGTTATTAA 2844  
  
QY   497  agaacatggacagttttaagaaaaaaaataactaaaaagttccaaaaaatgtgttaaag 556  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
DB   2843  ATAGTTTTGAACGCCGGAATTCGTTCAAAGTGCGCTTGGCTTTAAAGCGAGGTACGACAG 2784  
  
QY   557  ttcgtttctatctaagaatgaaatgccgatcttcogtcaaatttatggaagatactacag 616  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
DB   2783  TAGAACGATCTGATAGAAAGGTTTAAAAACAATTTGCTGAGTTATGAAATCATCTGGG 2724  
  
QY   617  agaagaaagattccaacgatcgtggcgatgactctctattacaatagataaaatccttg 676  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
DB   2723  AACGCGATGGCTTCTTAAACCGTGATATTAGTTACTTTGAAATATATTTATGATCGGTGC 2664  
  
QY   677  aaatgtaaaagatccctttagatatatagactttgaaaccttacattcccacaattagaaa 736  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
DB   2663  ATGAAGATGGAGATGCTGAACTATTTTGTATTAAGTTGGATCCAAAGAANAATATACGA 2604  
  
QY   737  agaacatgaacaatacaacaagaatattgcacaaagctgaaaagatttagaaaaga--- 793  
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy	794	-----aaccagataatcaaaaaacgattataaaatatagacaactttaaaacaacaaa	844
Db	2543	AAACATCTGAAAGACGACTAAAAAGCGCAAAATATGATTATGATCGCAAAATAAA	2484
Qy	845	gagaagaacaatgaagtaaatatagaagaagcacttcaactacacaagaacaatggtgata	904
Db	2483	TTGCTAAAATATGAAGATTAAACGAGACCTTAGAAGCTTTAGAAAGGAACATCCTGAAG	2424
Qy	905	cattaccaatagacagctggtttctttatttaataccattggaagttgtatatattacag	964
Db	2423	GTATTATCTTCTGTGCGCATTTAATAGTTTGTGCTCAAAATCATATTACTTATATG	2364
Qy	965	gtggttcaatogaatgaatatcgtcaacttgcagtagttgcaattcagtggggaatga	1024
Db	2363	GTGCGTCTCTTAATGAATTTAGAGATTTTTTACCAATCATATATGCAAGTATACGATGA	2304
Qy	1025	ttaataacggttagatcacacaattgcacggttataacttctatggtatcagcgaggact	1084
Db	2303	TGAGTATGCACTGACATGFGCAACAACCTTACGATTTCCGGTGCAGATAATGATC	2244
Qy	1085	tctcagaagatgcacctgctgttgcggtattataatttaaaagggttacaatgcagtg	1144
Db	2243	CAGATAAAGACTCAGACATATTGGATTATGGCATTTAAAAAAGTGTGGGAACTACT	2184
Qy	1145	tttatgaatatattggtgatttcgttaaaccaattataaacacagcgttacaagcatata	1204
Db	2183	TAAGTGAANAAGATTGGTGAATTTGATTATGTATGTAATCAGCCATTGTCCCAATTAATTG	2124
Qy	1205	caacactaaaaaagtataaaaaataaattgatt	1239
Db	2123	AGCAAGCTTAACCGCGTTTAAACAAAAGCTTAAAT	2089

Search completed: June 20, 2002, 12:04:14
Job time: 20969 sec

Fri Jun 21 08:38:26 2002

us-09-509-234c-50.rni

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:26:57 ; Search time 8551.36 Seconds
(without alignments)
2026.589 Million cell updates/sec

Title: US-09-509-234c-50
Perfect score: 1284
Sequence: 1 acatgaattgaagcttt.....tatgaattacagaggttaa 1284

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	95.8	7.5	990	12	CNS00601
C 2	94.2	7.3	982	12	AQ325799 nxb0021B
C 3	91.2	7.1	1042	12	CNS0148K
C 4	90.8	7.1	1059	12	CNS0022B
C 5	90.4	7.0	879	12	CNS01JRG
C 6	90.4	7.0	1101	12	CNS0021J
C 7	88.6	6.9	788	3	BI645011
C 8	88.6	6.9	910	10	BM415636
C 9	87.4	6.8	614	12	CNS0152H
C 10	87.4	6.8	796	12	AG077527
C 11	87.4	6.8	804	12	CNS001T2
C 12	87	6.8	1101	12	CNS000SX
C 13	86.8	6.8	1101	12	CNS01472
C 14	86.4	6.7	1025	12	CNS01472
C 15	86.4	6.7	1036	12	CNS00599
C 16	86	6.7	974	12	CNS001TT
C 17	84.8	6.6	1101	12	CNS0153V

18	84.4	6.6	778	12	AG058257
C 19	84.4	6.6	1101	12	CNS017V2
C 20	84	6.5	966	10	BM415686
C 21	83.8	6.5	934	12	AZ184244
C 22	83.8	6.5	967	12	CNS0772W
C 23	83.8	6.5	1101	12	CNS017Y0
C 24	83.6	6.5	830	3	BI645072
C 25	83.4	6.5	968	12	AQ687544
C 26	83.2	6.5	796	12	CNS0118D
C 27	83.2	6.5	875	12	AZ184435
C 28	83	6.5	1885	10	BE420745
C 29	82.8	6.4	922	12	AZ548363
C 30	82.6	6.4	834	12	BI2387
C 31	82.6	6.4	855	12	AZ183849
C 32	82.6	6.4	907	12	CNS021J4
C 33	82.6	6.4	1101	12	CNS012JN
C 34	82.4	6.4	688	9	AL514901
C 35	82.4	6.4	763	12	AG040720
C 36	82.4	6.4	850	12	AZ186328
C 37	82.4	6.4	1101	12	CNS00LJT
C 38	82.2	6.4	737	12	CNS008BU
C 39	82.2	6.4	833	12	CNS007X3
C 40	82	6.4	1135	12	CNS033GQ
C 41	81.8	6.4	773	3	BI644474
C 42	81.8	6.4	781	12	AG171177
C 43	81.8	6.4	947	10	BM416081
C 44	81.6	6.4	942	12	CNS018GS
C 45	81.6	6.4	963	12	CNS00A4L

ALIGNMENTS

RESULT 1
CNS00601/c
LOCUS
DEFINITION

CNS00601 990 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BAC14J23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AL065624
AL065624.1 GI:4944693
GSS:
fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

AUTHORS

TITLE

JOURNAL

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1..990
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"

Page 2

Query Match	7.5%;	Score 95.8;	DB 12;	Length 990;
Best Local Similarity	41.4%;	Pred. No. 0.00013;		
Matches 325;	Conservative	56;	Mismatches 401;	Indels 3;
				Gaps 2

[illegible]

50

399 AAAN 340
 Db
 690 tccttagcatatagacttgaaacttacattccacattagaaagaaagacatgaaca 749
 QY
 339 AA 280
 Db
 750 atacaagaagattgcagaagctgaagaagatttagaagaagaaacacagataatcaaaa 809
 QY
 279 AA 220
 Db
 810 aacgatttaataatagacacttaaacacaaagagaagacaaatgaactaaattaga 869
 QY
 219 AA 160
 Db
 870 agaagcacttcaactacacaaagaca 896
 QY
 159 AA 133
 Db

RESULT 6
 CNS0021J 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL061936 GI:4940214
 VERSION AL061936.1
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammos in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 PI and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 FEATURES
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 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR05N11"
 /note="end : TET3"
 BASE COUNT 631 a 7 c 28 g 289 t 146 others
 ORIGIN

Query Match 7.0%; Score 90.4; DB 12; Length 1101;
 Best Local Similarity 41.9%; Pred. NO. 0.00074;
 Matches 320; Conservative 32; Mismatches 411; Indels 1; Gaps 1;
 QY 510 tttaagaaagaaatactaaagctgtaaaagctgtaaaagctggtttctatc 569
 Db 102 TTTAATTAAAKAKNDTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 161

570 taaagatgaatgccgattccgtcaattatggaagatctactacagagaagaagattt 629
 QY
 162 AA 221
 Db
 630 caacgatcgtggagatgactcttattacaatagattaaatcttggaaatgtaagat 689
 QY
 222 AA 281
 Db
 690 tccttagcatatagacttgaaacttacattccacattagaaagaaacacatgaaca 749
 QY
 282 AA 341
 Db
 750 atacaagaagattgcagaagctgaagaagatttagaagaagaaacacagataatcaaaa 809
 QY
 342 AA 401
 Db
 810 aacgatttaataatagacacttaaacacaaagagaagacaaatgaactaaattaga 869
 QY
 402 AA 461
 Db
 870 agaagcacttcaactacacaaagaca 929
 QY
 462 AA 521
 Db
 930 tattattacccattgaagttgttatattatgcaggtggttcacgaatgaatcgcaca 989
 QY
 522 TAWTTTTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 581
 Db
 990 ctttcagcgtgattatgcattcagtggaagattgaatacgcgttagatcacacacat 1049
 QY
 582 ATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 640
 Db
 1050 tgacggttataactctctatggtatcagcgcagcactctcagaagatgcacctgattgg 1109
 QY
 641 TTTTWTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 700
 Db
 1110 cgttattaaattaaagaggttacatgcagatgttatgaatatattggtgattcgt 1169
 QY
 701 WTTTTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 760
 Db
 1170 taaacaaatttaaacaccagcgtcaagaagacatacacacataaaagattattaaaaa 1229
 QY
 761 AWAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 820
 Db
 1230 ataaatgatttcagtagagaggaatttagaataatgaatt 1273
 QY
 821 AAWAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 864
 Db

RESULT 7
 BI645011/c
 ID BI645011 standard; RNA; EST; 788 BP.
 XX
 AC BI645011;
 XX
 SV BI645011.1
 XX
 DT 13-SEP-2001 (Rel. 59, Created)
 DT 13-SEP-2001 (Rel. 59, Last updated, Version 1)
 XX
 DE OP2810 Mixed Stage EST's from Globodera pallida, the potato cyst nematode
 DE Globodera pallida cDNA, mRNA sequence.
 XX
 KW EST.
 XX
 OS Globodera pallida
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
 XX
 RN [1]
 RP Heer J., Sosinski B., Pokrzywa R.M., Wary A., Opperman C.;
 RA "Mixed Stage EST's from Globodera pallida, the potato cyst nematode";
 RT


```

Query Match      6.8%; Score 87.4; DB 12; Length 614;
Best Local Similarity 49.8%; Pred. No. 0.0023;
Matches 215; Conservative 9; Mismatches 205; Indels 3; Gaps 1;

QY 813 gattaataaataagacacttaaaacaagaagaagcaaaatgaagctaaatagaaga 872
Db 600 AAAAAAANAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 544
QY 873 agcacttaactacaacaagaacatggtgtacattaccatgcgcgtggtctttat 932
Db 543 AANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 484
QY 933 tattaatccattgaagttgtattatgcaggtggttcacgcgaatgcactt 992
Db 483 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 424
QY 993 tgcaggtgtatgcattcagtggaatgattacacgcgttagatcacacattga 1052
Db 423 AANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 364
QY 1053 csgttataacttctatggtatcagcgagactctcagaagatgcactgattg 1112
Db 363 NNTNNNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTT 304
QY 1113 tattaatttaaaagtggtacatgcagtggttgcagttatggtatttcgttaa 1172
Db 303 TTTTTCCTCCCAAAAAAANAANAANAANAANAANAANAAGCGGGGGTGTGTTTTTAA 244
QY 1173 accaattataaccagcgtacacagcatatacacactaaataagattataaataa 1232
Db 243 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 184
QY 1233 aatgatttcagtaagaggaatttagataatgaaattttacagagtt 1282
Db 183 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAAGCT 134

RESULT 9
CNS0152H 614 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN12N03 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL104915
VERSION AL104915.1 GI:5616929
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
REFERENCE 1 (bases 1 to 614)
AUTHORS Drosophila melanogaster
TITLE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
JOURNAL Genoscope.
COMMENT Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.
FEATURES
source Location/Qualifiers
1..614
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN12N03"
/notes="end : SP6"
BASE COUNT 553 a 0 c 0 g 41 t 20 others
ORIGIN

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Query Match      6.8%; Score 87.4; DB 12; Length 614;
Best Local Similarity 49.8%; Pred. No. 0.0023;
Matches 215; Conservative 9; Mismatches 205; Indels 3; Gaps 1;

QY 468 agaaagatggaagaagaagcctcatcagaacacatggacagcttttaagaaaaagaatac 527
Db 37 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 96
QY 528 taaaaagttcaaaaaaagggtttaagttcgtttttctctctaaagatgaaatgcgcgt 587
Db 97 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 156
QY 588 ---attcgcgtcaatttatggaagactacacagagaagaagatttcaacgatcggtgcga 644
Db 157 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 216
QY 645 tgacttctattacaatagattataaatactttgaaatgttaagattccttttagcatat 704
Db 217 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 276
QY 705 agacttgaacttcaattcacacattagaagaagaacatgaacatacaacaagatat 764
Db 277 AAWATAAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 336
QY 765 tgcagaagctgaagaagatttagaagaagaacacagataatcaaaaaacgattcaataa 824
Db 337 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 396
QY 825 agacaacttaaaacaacaagaagaagaatgaagctaaattgagaagaagcacttcaact 884
Db 397 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 456
QY 885 acaacaagaaca 896
Db 457 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 468

RESULT 10
AL524807/c
LOCUS AL524807 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC008YK01 3
DEFINITION prime, mRNA sequence.
ACCESSION AL524807
VERSION AL524807.1 GI:12788300
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 796)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source Location/Qualifiers
1..796
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC008YK01"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Penq Lianq Life

```

<http://fulllength.invtrogen.com>

```

clone tracking errors.
PRIMERS
Sequenceing: -21M13
LIBRARY
Vector      : pKS145
R.site 1    : SacI
R.site 2    : SacI.
location/Qualifiers

```

Source

BASE COUNT	467 a	0 c	1 g	0 t	316 others
ORIGIN	/cellar/qpc sim1 /clone_11b="PTB Chimpanzee Male BAC Library				

ORIGIN

Best Local Similarity	29.0%	freq: no: 0.00%	Indels	0	
Matches	229;	Conservative	0;	Gaps	0
			Mismatches	545;	

Mathematics

—

—

105 217

20

1.85 AF

746 aē

243 AM

— 3 —

•

338

AAS

1046 a

545 P

1106 t

609

44

•

Search completed: June 20, 2002, 14:27:04
Job time: 17734 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:12:45 ; Search time 12428.6 Seconds
(without alignments)
2183.803 Million cell updates/sec

Title: US-09-509-234C-48
Perfect score: 1297
Sequence: 1 acgacggcgaattggcgc.....tatgaattacagagtaa 1297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	1297	100.0	1297	6	A97492	A97492 Sequence 48
2	1248	96.2	1266	1	AF099967	AF099967 Staphyloc
3	825.6	63.7	1266	1	AF144662	AF144662 Staphyloc
4	722.6	55.7	1371	6	A97497	A97497 Sequence 53
5	722.4	55.7	1350	1	SSV12875	Y12875 Staphylococ
6	704.4	54.3	1257	1	AF144663	AF144663 Staphyloc
7	703.4	54.2	1295	6	A97488	A97488 Sequence 44
8	700.2	54.0	1260	1	AF145333	AF145333 Staphyloc
9	699.6	53.9	1263	1	SD66880	U66880 Staphylococ
10	698.8	53.9	1263	1	AF099965	AF099965 Staphyloc
11	684.8	52.8	1263	1	AF145332	AF145332 Staphyloc
12	681	52.5	1343	1	SHV12874	Y12874 Staphylococ
13	681	52.5	1343	6	A97496	A97496 Sequence 52
14	674	52.0	4434	6	AX145015	AF269697 Staphyloc
15	674	52.0	4434	6	AX145015	AX145015 Sequence
16	672.4	51.8	1877	6	A97490	U23713 Staphylococ
17	670.6	51.7	1283	6	A97490	AF9490 Sequence 46
18	668.6	51.5	1254	1	AF099964	AF099964 Staphyloc
19	666.4	51.4	1257	6	I32344	I32344 Sequence 1
20	658.8	50.8	3446	1	SAFEA	X17688 S.aureus fa
21	657.2	50.7	303750	1	AP003133	AP003133 Staphyloc
22	657.2	50.7	346900	1	AP003362	AP003362 Staphyloc
23	652.6	50.3	1305	6	A97484	AF099962 Staphyloc
24	649	50.0	1263	1	AF099962	AF099962 Staphyloc
25	649	50.0	1263	1	SHU23711	U23711 Staphylococ
26	648.2	50.0	1263	1	AF144661	AF144661 Staphyloc
27	645.6	49.8	1280	6	A97486	A97486 Sequence 42
28	644.2	49.7	1260	1	AF099963	AF099963 Staphyloc
29	635	49.0	1179	6	AX141471	AX141471 Sequence
30	601.6	46.4	1284	6	A97494	A97494 Sequence 50
31	596.6	46.0	1254	1	AF099966	AF099966 Staphyloc
32	589.2	45.4	1328	6	A97445	A97445 Sequence 1
33	386	29.8	3115	1	AF269316	AF269316 Staphyloc
34	386	29.8	3115	6	AX144636	AX144636 Sequence
35	347.8	26.8	1551	1	AF106849	AF106849 Staphyloc
36	347.8	26.8	297850	1	AP003137	AP003137 Staphyloc
37	347.8	26.8	341350	1	AF003365	AF003365 Staphyloc
38	338.4	26.1	54064	2	AC090968	AC090968 Staphyloc
39	311.8	24.0	1805	1	AF093750	AF093750 Staphyloc
40	311.2	24.0	2558	1	AB000222	AB000222 Staphyloc
41	310	23.9	6528	1	SSU66883	U66883 Staphylococ
42	282.8	21.8	4140	1	AB015195	AB015195 Staphyloc
43	278	21.4	34735	1	AF003361	AF003361 Staphyloc
44	276.4	21.3	2816	1	AF106851	AF106851 Staphyloc
45	250.6	19.3	1260	1	SHU23712	U23712 Staphylococ

ALIGNMENTS

RESULT	1	A97492	Sequence 48 from Patent WO9916780.	DNA	linear	PAT 26-JAN-2000
LOCUS	A97492	Sequence 48	from Patent WO9916780.	DNA	linear	PAT 26-JAN-2000
DEFINITION	A97492	Sequence 48	from Patent WO9916780.	DNA	linear	PAT 26-JAN-2000
ACCESSION	A97492	Sequence 48	from Patent WO9916780.	DNA	linear	PAT 26-JAN-2000
VERSION	A97492.1	GI:6780838		DNA	linear	PAT 26-JAN-2000
KEYWORDS		Staphylococcus schleiferi.		DNA	linear	PAT 26-JAN-2000
SOURCE		Staphylococcus schleiferi.		DNA	linear	PAT 26-JAN-2000
ORGANISM		Bacteria; Firmicutes; Bacillus/Clostridium group; Staphylococcus.		DNA	linear	PAT 26-JAN-2000

REFERENCE 1 (bases 1 to 1297)
Gala, J. and Vannuffel, P.
GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
Patent: WO 99/16780-A 48 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)

FEATURES
source
1..1297
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BASE COUNT      495 a      184 c      249 g      369 t
ORIGIN

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Query Match      100.0%: Score 1297; DB 6; Length 1297;
Best Local Similarity 100.0%: Pred. No. 2e-212;
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS      Staphylococcus schleiferi factor essential for methicillin
DEFINITION      resistance fEma (fema) gene, complete cds.
ACCESSION      AF099967
VERSION      AF099967
KEYWORDS      AF099967.1 GI:3820633
SOURCE      Staphylococcus schleiferi.
ORGANISM      Staphylococcus schleiferi.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE      1 (bases 1 to 1266)
AUTHORS      Vannuffel, P., Heusterspreute, M., Bouyer, M., Philippe, M. and Gala
J.-L.
TITLE      Molecular characterization of fema from Staphylococcus hominis,
Staphylococcus saprophyticus and Staphylococcus haemolyticus and
fema-based discrimination of staphylococcal species
JOURNAL      Res. Microbiol. (1998) In press
REFERENCE      2 (bases 1 to 1266)
AUTHORS      Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE      Direct Submission
JOURNAL      Submitted (21-OCT-1998) IBCN, UCL, Clos Chapelle-aux Champs
30/3046, Bruxelles 1200, Belgium
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	EFRRFAGSYAQVEMINFTAYDIQIPIRYFISGDSFSEDAEDAGVKEFKKGYNAEVIE		
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ORIGIN			
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Best Local Similarity	100.0%; Pred. No. 4.6e-204;		
Matches 1248; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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QY	61 gtagggaactgaattaaaggctgctgaaggctgtgaacaacatctctcgccatcaaa 120		
DB	79 GTAGGGAACTATGAATTTAAAGGTCGTGAAGGTGTTGAACACACATCTTTCGGCATTTAA 138		
QY	121 gatacaacaatacgtactacgacgctgtttactgacagcagtcgacagtaaatgaattt 180		
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QY	181 tttaaatattttttattcaaacgcggaccagcttcaggactcgaataaaacagctgctt 240		
DB	199 TTTAAATATTTTATTCAAAACCGCGACAGTCATGGACTACGAAATAAAGAGTCGTT 258		
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DB	259 CATTTCTTTTAAATGAACATTTCAAAATATGCTTAAGAAATATCACGCATTTGTTTGA 318		
QY	301 gtacaccttatttaccaatgtttaagcgaaaccatgatggtgaagtgattgaagatac 360		
DB	319 GTAGACCTTTATTTACCAATGTTAAAGCGAAACCATGTTGTAAGTGTGTAAGATGATG 378		
QY	361 ggcagtgactggttttttgataaaatggctgaattaaactttgaacatgaaggtttcaca 420		
DB	379 GCGAGTGACGTGGTTTTTGTATTAANTGCTGAATTTAACTTTGAACATGAAGGTTTCAG 438		
QY	421 actgggttgatatacaataaggcaaatctgtttcatctgtgctgattgtgaaataaa 480		
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QY	481 aaatcaaaagaacatctaaatcaaatggataattttaaggaagaaataacgaaaaagta 540		
DB	499 ACATCAAAAGACATCTTAAATCAATGGATATTTTAAGGAAAAAGAAATACGAAAAAAGTA 558		
QY	541 cagaaaaatgggtgaagctcgcgtacttaaacggaagatgaatacatattttccgtctg 600		
DB	559 CAGAAAAATGGTGTGAAGTCGCGTATCTTAAACGAAGATGAATTTACATATTTCCGTCG 618		
QY	601 ttatctggaagatacatctgaacaaaagattttgtagatagagatgacgatttttatat 660		
DB	619 TTTATGGGAAGATACATCTGAAACAAAGAGATTTGTAGATAGAGATACGATTTTATTAT 678		
QY	661 catcgtatgaataactataaagatcgtgtccgcgtacacactagcgtatttgatttaat 720		
DB	679 CATCGTATGAAATACTATAAAGATCGTGTCCGCGTACACACTAGCGTATATTTGATTTAAT 738		
QY	721 gcatatttagcaggtcacaactcgaagcgaagacttttaaaaaagaataatgcgaagca 780		
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ORIGIN

Query Match      63.7% Score 825.6; DB 1; Length 1266;
Best Local Similarity 78.8%; Pred. No. 7,3e-132;
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Db 79 GTAAGGACATTCAGAGCTTAAAGTGGCAGAGGTTCGAAACACATCTGTCGGTATTA 138

QY 121 gataacaacaatacgtactagcaagcatgttactgacagcagtgccagtaagatt 180
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QY 1141 aatgcagaagataagaataatgctggtgatttatttaagcctataaacaacctgc 1200
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QY 1201 acagctacttaataaataaagaacaaataaagaacgaagataaagaataa 1248
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LOCUS Sequence 53 from Patent WO916780.
DEFINITION A97497
ACCESSION A97497
VERSION A97497.1 GI:6780844
KEYWORDS
SOURCE
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Staphylococcus saprophyticus.
Staphylococcus saprophyticus
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
1 (bases 1 to 1371)
Gala,J. and Vannuffel,P.
GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
TITLES
GENETICS FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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BASE COUNT      545 a      155 c      248 g      423 t
ORIGIN

Query Match      55.7% Score 722.6; DB 6; Length 1371;
Best Local Similarity 73.2%; Pred. No. 2,9e-114;
Matches 942; Conservative 0; Mismatches 339; Indels 6; Gaps 1;

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Qy	70	tatgaattaaaggttgcgtgaaggtgttgaacacacatcttgcgcatcctaagaacaac	129
Db	1231	GTAGTAGAATATGTTGGTGAATTTTAAACCGGATTAATAAGCCAAATGTACAAAATTTAT	1290
Qy	1210	ttaaattaaagcaattaaagacagataaaaagataagaataagataagcaagagaagggga	1269
Db	1291	ACGATTTGAAAAATTAAGGATAAAAGAAATAAACATAATAG-----AAGGAAAC	1344
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Db	1345	TAAAGCTAGAATGAATTTTACAGAGTTA	1371
RESULT	5		
SSV12875			
LOCUS	SSV12875	1350 bp	DNA
DEFINITION	Staphylococcus saprophyticus fema gene.		
ACCESSION	Y12875		
VERSION	Y12875.1	GI:2462696	
KEYWORDS	fema gene.		
SOURCE	Staphylococcus saprophyticus.		
ORGANISM	Staphylococcus saprophyticus		
REFERENCE	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.		
AUTHORS	1 (bases 1 to 1350)		
JOURNAL	Vannuffel, P.		
REFERENCE	2 (bases 1 to 1350)		
AUTHORS	Direct Submission		
JOURNAL	Submitted (30-APR-1997) P. Vannuffel, University of Louvain Medical School, Laboratoire de Genetique Moleculaire, UCL-GENO-5225, Avenue F. Mounier 52, Brussels, 1200, BELGIUM		
COMMENT	Y12875 incorrectly cited in: Science: 276: 2054-2057 (1997).		
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BASE COUNT	535 a 154 c 244 g 417 t		
ORIGIN			
Query Match	55.7%	Score 722.4;	DB 1; Length 1350;
Best Local Similarity	73.6%;	Pred. No. 3.1e-114;	
Matches	921; Conservative	0; Mismatches 331;	Indels 0; Gaps 0;
Qy	10	gaatttggtgcgtttacagatcaaatgcaatagccattccacgaatgtagggaac	69
Db	92	GAGTTCGGTGATTTACGGATAAAATGCGGAATAGTCAATTTTACGCAATAGTTGGAAAT	151

Oy 70 tatgaatlaaagttcgtcgaagtggtgaaacacacttctgcgcgttaagaacac 129
 Db 152 TATGAATGTAATTCGAGAAATGACGAAACACCTAGTAGATATTAAGATATAT 211
 Oy 130 aataagclactagcagcagcttctacgagcagcagcagcagcagcagcagc 189
 Db 212 AATGAAGTATTCGACGATGTTTACTTACGCTGTTCCGTATGAAGTATTCAG 271
 Oy 190 tttatccaacccgagccagtcagtcagtcagtcagtcagtcagtcagtcag 249
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 Oy 250 tttatgaacttcaaatatgtaagaatatacagcagcagcagcagcagcagc 309
 Db 332 TTTAACGATTTACGAAATATGTAATTAATTAATTAATTAATTAATTAAT 391
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 Db 392 TATCTGCTTATCATATATGTAATGTAATGTAATGTAATGTAATGTAATG 451
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 Db 632 GGGTGAAGTAAATTTTATGATGATGATGATGATGATGATGATGATGAT 691
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 Db 1112 ATTAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1171
 Oy 1090 ttttgaagaatgcagaagcagcagcagcagcagcagcagcagcagcagc 1149
 Db 1172 TTTACTGAAGTGAAGATGCAAGTGTGTAAATTTAAAGGTTTAAATGCA 1231
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Db 1232 GTAGTAGAATATGTTGATTTTAAACCGATTAAACCAATTAATTAAT 1291
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RESULT 6
 AF144663 1257 bp DNA linear BCT 01-JUN-1999
 LOCUS Staphylococcus warneri factor essential for methicillin resistance
 DEFINITION (femA) gene, complete cds.
 ACCESSION AF144663
 VERSION AF144663.1 GI:4929302
 KEYWORDS Staphylococcus warneri.
 SOURCE Staphylococcus warneri.
 ORGANISM Bacteria; Firmicutes; Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1257)
 AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
 TITLE Cloning and characterization of femA genes from Staphylococci
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1257)
 AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-1999) LBCN, UCL 3046, Clos Chapelle-aux-Champs,
 30, Bruxelles 1200, Belgium
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BASE COUNT 481 a 183 c 213 g 380 t
 ORIGIN

Query Match 54.3%; Score 704.4; DB 1; Length 1257;
 Best Local Similarity 73.4%; Pred. No. 3.8e-111;
 Matches 900; Conservative 0; Mismatches 326; Indels 0; Gaps 0;

Db 10 gaattggtggtttaaagcagcagcagcagcagcagcagcagcagcagcagc 69
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 Db 88 TATGAATTAAGTGAAGATGCAAGTGTGTAAATTTAAAGGTTTAAATGCA 147
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REFERENCE 1 (bases 1 to 1260)
AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE Cloning and characterization of femA genes from Staphylococci
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1260)
AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE Direct Submission
JOURNAL Submitted (23-APR-1999) IBCU, UCL 3046, Clos Chapelle Aux Champs,
30, Bruxelles 1200, Belgium
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Best Local Similarity 73.0%; Pred. No. 2e-110;
Matches 900; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
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RESULT 8
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LOCUS Staphylococcus cohnii subsp. urealyticum methicillin resistance
DEFINITION protein FemA (femA) gene, complete cds.
ACCESSION AF145333
VERSION AF145333.1 GI:5565908
KEYWORDS Staphylococcus cohnii subsp. urealyticus.
SOURCE Staphylococcus cohnii subsp. urealyticus
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group;

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Fri Jun 21 08:38:22 2002

staphylococcus
Mol. Microbiol. 23 (6), 1251-1265 (1997)
97260121
2 (bases 1 to 1263)
Thumm, G. and Goetz, F.
Direct Submission
Submitted (13-AUG-1996) Mikrobielle Genetik, Universitaet
Tuebingen, Waldheuser Strasse 70/8, Tuebingen 72076, Germany
Location/Qualifiers
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JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

gene

CDS

BASE COUNT 470 a 191 c 241 g 361 t
ORIGIN

Query Match 53.9%; Score 699.6; DB 1; Length 1263;
Best Local Similarity 72.7%; Pred. No. 2.5e-110;
Matches 903; Conservative 0; Mismatches 339; Indels 0; Gaps 0;
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QY 61 gtagggaactataaataaaggctgcaaggggtggaacacacattctgtcgcaataa 120
Db 79 GTAGGCAACTATGAGTTGAAAGTTGCGAGAGGTACAGAAACACATCTTGTGCGGGTGA 138
QY 121 gatacaacaataacgtactagcagcatgtttactgacagcggtgccaagtaagaatt 180
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QY 181 tttaaatatttttttatacaacggcgaccagctcagctacgacgaaataaagagctggt 240
Db 199 TTTAAATATTTCTATTCAAACCGGTGGCGGCTCATTCATTATGATTAATAAGAATTAGTC 258
QY 241 cattcttttttaagaaactttcaaaatattgttaagaataatatacagcattgtattgaga 300
Db 259 CATTTCTTTTGTAGAAATTAAGGCATATGTTAAACAATACAATGCATTACTTACTAAGA 318
QY 301 gttagccctttttaccattgttaagcgaaacccatgattggtgaagtgtgaagatac 360
Db 319 GTAGATCCATATTTACCATATCAATACCGTAACCATGATGTTGAGATTACAGAAATGCA 378
QY 361 ggcagtgactggttttttgataaaaaggctgaattaaacttgaacatgaaggtttcaca 420
Db 379 GGTGATGATGGATATTTGATAAAATGGAAACAAATGGGTTATATATCCATCAGGCTTTACA 438
QY 421 actgggttgatacaataaaggcaaatctgtttcattctgtctgctgattgtgataaataa 480
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QY 430 gatacaataagcgcaaatcttttcoattctgtgctgctgattgaaataaacaacataa 489
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QY 670 aaatactataagatgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 729
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QY 730 gcagagctcaacatgaagcgcaagacttttaaaaaagaatttgcagaagcagataaagac 789
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QY 850 ctgaagcgcaatcaaatcaataaagaacagcaaacatctgcaactcaaacacggtgac 909
Db 868 CTTATTGCAATCAACAAAGATGATGAAGCTAAATCATTTACAGAACACACACGCTAAT 927
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Db 928 GAATTTACCAATTTTACGAGCAGTCTTTATCGTCAATCCATCAACGAGTAGTATTATGCG 987
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Db 1108 TTTTTCAGAGCAGCAGAGATGCGAGGTGTTGTGAAGTTTAAAGAGGATTCACGCTGAT 1167
QY 1150 gtaataagaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctac 1209
Db 1168 GTAGTTGAATATGTTGTTGATTTTATAAACCACATCAATTAAGCCAAATGTACAAAATTTAT 1227
QY 1210 ttaaaattaaagcaataaagacacataaaa 1242
Db 1228 ACATGTTAAGGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1260

RESULT 9
SSU66880 1263 bp DNA linear BCT 25-APR-1997
LOCUS SSU66880
DEFINITION Staphylococcus simulans femA (femA) gene, complete cds.
ACCESSION U66880
VERSION U66880.1 GI:1762961
KEYWORDS Staphylococcus simulans.
SOURCE Staphylococcus simulans
ORGANISM Staphylococcus simulans
Bacteria; Firmicutes; Bacillus/Clostridium group;
REFERENCE 1 (bases 1 to 1263)
AUTHORS Thumm, G. and Goetz, F.
TITLE Studies on polysostaphin processing and characterization of the
lysostaphin immunity factor (Lif) of Staphylococcus simulans biovar

Db 499 ACACCAAGATGTTTAAAGGTATGATGCTACGTAACCTAATATAGAAAAAGTA 558
 Qy 541 cagaagaatgctggaagtcgctatcaacgaagaatgaattacatttcgctcg 600
 Db 559 AAGCGTATGCTGTAAGTACCGCTCTGTAGTGAAGATGAATGATATTTCCCTAAA 618
 Qy 601 ttatggaagatacatcctgaaacaaagatttctgataagagatgacgattttat 660
 Db 619 TTTATGGAAGTACGACAGACGAAAGACTTTGATGATCGTGAAGAGACTTCTATT 678
 Qy 661 catgtatgaatacatataaagatgctgctcgccactgacactgctatatttaac 720
 Db 679 CACAGACTAAACACTATTAATGATGATGCTGATGATGATGATGATGATGATGAT 738
 Qy 721 gataatgagagctcaacactgaaagcgaagacttaaaagaagaatgcaaaagca 780
 Db 739 GATTATATTAATGATTAATGAAAGCTGACAAAGAAATTAAGAAATCAATTAAGCT 798
 Qy 781 gataagacatcgacaaagcgtctcaaaatcagaagccataataaagaagaattta 840
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 Qy 841 gagcaacactagaagagaaactcaaaataaagaagcgaagaacttgcaacttaa 900
 Db 859 GAACCAACTTGAAGCACTATCAAAAAGTTGCTGACGACGACGACGACGACGACG 918
 Qy 901 caagctgacacatcagacttgcgctgattctttatccatttgaagtggtt 960
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 Qy 1081 agtggatcttcagaaagatgacgaagatgacagtgatgataaataaagaagctat 1140
 Db 1099 AGCGGACACTTGAAGAGCGTGAAGAGCGAGCGCTGTGAAGTTCAAAAAGATTT 1158
 Qy 1141 aatgcaagaatgaataatgctgctgatttataaagcctataaacaacctgacct 1200
 Db 1159 AACGCAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1218
 Qy 1201 acagctacttaaaatlaaagcaattaaagaagaataaana 1242
 Db 1219 AACCTTATACAGCTTAAAGAAATCAAGATGATTAAC 1260

RESULT 10
 AF099965 1263 bp DNA linear BCT 02-NOV-1998
 LOCUS AF099965
 DEFINITION Staphylococcus xylosus factor essential for methicillin resistance
 FEWA (fema) gene, complete cds.
 ACCESSION AF099965
 VERSION AF099965.1 GI:3820629
 KEYWORDS
 SOURCE Staphylococcus xylosus.
 ORGANISM Staphylococcus xylosus
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1263)
 AUTHORS Vanuifel,P., Heusterspreute,M., Bouyer,M., Philippe,M. and Gala
 J.-L.
 TITLE Molecular characterization of fema from Staphylococcus hominis,
 Staphylococcus saprophyticus and Staphylococcus haemolyticus and
 fema-based discrimination of staphylococcal species
 JOURNAL Res. Microbiol. (1998) In press
 REFERENCE 2 (bases 1 to 1263)
 AUTHORS Vanuifel,P., Heusterspreute,M. and Gala,J.-L.

TITLE Direct Submission
 JOURNAL Submitted (21-OCT-1998) LBCW, UCL, Clos Chapelle-aux Champs
 30/3046, Bruxelles 1200, Belgium
 FEATURES
 source Location/Qualifiers
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 KKAVNKDNLEKOLIANOOKIDEAKTLOEKHGNELPISAAYFIINPEVYVYAGTSH
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 BASE COUNT 496 a 151 c 236 g 380 t
 ORIGIN

Query Match 53.98; Score 698.8; DB 1; Length 1263;
 Best Local Similarity 73.08; Pred. No.3,4e-110;
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 Qy 13 ttgtgctgttcaacagataaagccatagacattcaacgcaaatggttaggaacct 72
 Db 31 TTGGTGCACTTTACAGATTAATGCCAATATGCAATTCACGCAATAGTGAGGATTA 90
 Qy 73 gaattaaagcttcgaagtggttgaagaacacatctgtcgcgcatlaaagaatacaaat 132
 Db 91 GAATTGAAATTCACAAAGTACTGAAACACATTTGATGATGATGATGATGATGAT 150
 Qy 133 aacgtactagcagcatgttactagcagcagtgccagtaagaagttttaatat 192
 Db 151 GAACTCATTCGACCTGTTTATTATACAGTACAGTACAGTACAGTACAGTACAGT 210
 Qy 193 taltcaacgcgacccagctcatgacatcaagaataaagaagcgttcattcctttt 252
 Db 211 TATACTAATAGAGTCCGCTGTATGATTTGAAAAATTAAGAAATTAAGTATGAT 270
 Qy 253 aatgacttcaaaatgctgaagaataatcaacgcatctgattgagagtagaccttat 312
 Db 271 AATGAACATCTTAATATGTAAGAAATCAATACGCTTATTAATTAAGAGTTGAT 330
 Qy 313 ttaccaatglttaagcgaaacacatgagtgtgaagtgatgaagaatacggaagtgactg 372
 Db 331 TTGAGTATCAATACCGTAAATCATGATGATGATGATGATGATGATGATGATGAT 390
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 Qy 493 atcttaatacaatgataatgaagaagaataacgaaataaagaatacaagaataagtt 552
 Db 511 GTACTAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 570

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QY	553	gtgaagtcgcgtctctaaacgaagatgaattacatatatttcctggttcgtttatgaagat	612
Db	571	GTGAAAGTAAGGTTCTTAAAGGAAGATGAGTTGGCAATTTTCGTTTCATTCATGGAAGAT	630
QY	613	acatctgaacaaagatttttagatagatgacgattttttattatcatcatgataaaa	672
Db	631	ACATCTGAACCTTAAGACTTTGACGATAGAGACGATGCTTTTACTACATAGATTAGG	690
QY	673	tactataaagatcgtgcgcgtaccactagcgtatattgatttttaattatcatattagca	732
Db	691	TATNTAAGATCGCGTATTAGTACCTCTAGCTTATATGGATTTCATGAATATATTGAA	750
QY	733	gagctcaacacgaagcgaagactttaaaagaatgcaaaagcagatgaagacatc	792
Db	751	GAATTCGAAGCTGAACGAGGCTTTAAGCAAGATATCAATAAAGCAGTAAAGATATC	810
QY	793	gacaagcgtcctgaaatacagaagccataataaaagaagaaatttagagcaacaacta	852
Db	811	GAGAAAGACCTGAAATATAAAGACATATAATAAAGAGATAATCTAGAGAAACACTT	870
QY	853	gaagcgaatcaagctaaataaagaagcagaacattgcaacttaaacacgctgacaca	912
Db	871	ATAGGAATCAACAAAATGATGAAGCTTAAACCTCTACAGACGACATGCTAACGAA	930
QY	913	ttacogatttcggtgattcttatttaataatccattgaggtttgatttatgagcgc	972
Db	931	CTACCAATCTCAGACACATATTTATCATCTAATACCTTATGAAGTAGTATGCGGT	990
QY	973	ggcagcgaacgaatcttcgttcatttgcgtggaagcagcagtcgaatggaatgatt	1032
Db	991	GGAAGCTCARATGAGTTAGACATTTTCTGCTAGTTATGCCATCAATGAAGATGAT	1050
QY	1033	aatttcgattgattatcaaatccagatataactttatgctgattgagtgatttt	1092
Db	1051	AACATGCTATGATGACCAATATATGATAGATATATTTTATGGAATAGTGGTCA	1110
QY	1093	tcgaagatcgagagatgagcgtgtgatataaatttaaaagcgtatataatgcaagata	1152
Db	1111	ACAGAAGATGAGAGATGCGGTGATGATTAATTTAAAGAGATTAATGCGGATGTA	1170
QY	1153	atagaatgctggtgattttatgaacctataaacaacacgcctctacacgtctactta	1212
Db	1171	GTGGAATATGTTGGTATTTATTAACCAATCAATTAACCAATGATACAAATTTATACG	1230
QY	1213	aaattaagcaattaaagaacagataaaa	1242
Db	1231	ACATTAAAGAAATTAAGATATAAAGAAA	1260
RESULT	11		
LOCUS	AF145332	1263 bp	linear BCT 22-JUL-1999
DEFINITION	Staphylococcus gallinarum methicillin resistance protein Fema		
ACCESSION	AF145332		
VERSION	AF145332.1		
KEYWORDS	(fema) gene, complete cds.		
SOURCE	Staphylococcus gallinarum.		
ORGANISM	Staphylococcus gallinarum		
REFERENCE	Bacteria, Firmicutes; Bacillus/Clostridium group;		
AUTHORS	Vannuffel, P., Heusterspreute, M. and Gala, J.-L.		
TITLE	Cloning and characterization of fema genes from Staphylococcus		
JOURNAL	1 (bases 1 to 1263)		
REFERENCE	2 (bases 1 to 1263)		
AUTHORS	Vannuffel, P., Heusterspreute, M. and Gala, J.-L.		
TITLE	Direct submission		
JOURNAL	Submitted (23-APR-1999) LBCM, UCL 3046, Clos Chapelle Aux Champs,		
FEATURES	30, Bruxelles 1200, Belgium		
source	Location/Qualifiers		
	1 1263		

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	Best Local Similarity	72.2%; Pred. No. 8.5e-108;
	Matches	890; Conservative 0; Mismatches 342; Indels 0; Gaps 0;
QY	10	gaatttggtcgtttacagataaaatgccatattcagcatttcagcaaaatggtggaac 69
Db	28	GAATTCGGACATTTACAGATAGTATGCTTAATACCATTTCTACTCAATGCTGGGAAC 87
QY	70	tatgaattaaaggttgcgtgaaggtgttgaaacacatctctgcgcattaaagataaacac 129
Db	88	TATGAATTAATAATTTGCAGAGGTTACAGAAACACATTTAGTAGTATAAATAATGAA 147
QY	130	aataacgtactagcagcgtgttactgacagcagcgcagcgaatgaagtttttaaatat 189
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QY	190	ttttattcaacgcgacacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 249
Db	208	TTTTATCTACTAACCGTGGACCGGTAATAGATTTTGAATAAAGAACTGTGCAATCTTC 267
QY	250	tttatgaactttcaaaatattgttaagaataatcaacgattgtattgagagtagacct 309
Db	268	TTTAAATGAATTATCAAAATATGTAAGAAACATCGTGGCGCTTTATTTAAGAGTTGATCCA 327
QY	310	tatttaccatgtttaaagcaaacacatgattgtgaagtgattgaagaataaacaataaa 369
Db	328	TATTTACCTTACCAATATCGAATATCATGATGCTGATGATATAGAGAAATGCGAGGCATGAT 387
QY	370	tgggtttttgataaaatggctgaatttaaaactttgaacatgaagttttcaacacgtggtt 429
Db	388	TGGATCTTCGATAGATGAAGCATTTAGGTTATAACACACCAAGGTTTCTTAACTGGTTTT 447
QY	430	gatacaataagggcaaatctgttttcaattctgtctgattgaagaataaacaataaa 489
Db	448	GATCCAGTCGTTCAATAAAGATTTTCACTCAGTATTTAGAGTTAAGGATAAGACTGATAAG 507
QY	490	gacattttaaatgaatgataatttaaggaagaaataacgaataaagaataacagaaaaat 549
Db	508	GATGTCCTTAAAGACATGGATGTTTACGTAAAGCGAAGCACTAAACAAAGTTCAAAAAT 567
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Db	568	GGTGTAAAGTACGTTTCTTCTAGTGAAGATGAATGCCAATCTTTAGAGATTTATGGA 627
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[illegible]

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Db 802 GAATATCTTGAAGAAGCTTCATGCGAGACGTCAGACATTAATAAAGAGCTTAACAAAGCT 861
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 Db 862 CTAAGAATATTGAAAGACGACAGATAACAAAAGACACAAAATAAATAAATAATTA 921
 Qy 841 gacgaacacatgacgaagcgaatcaagctaaataaagaagcagagaacattgcaacttaaa 900
 Db 922 GAACAGCAATTAAGAAGCAATGAGCAAAAATTCATGAGAGCACACAACTTCAATTAGAA 981
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 Db 982 CATGTGACGAATTAACATATCTGCTGATTTCTTCTTATTATATCCATTGGAAGTTGA 1041
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 Qy 1021 tgggaatgattattatgcattgattatcaaatccaaattccaaagataataattttatggcatt 1080
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 Qy 1081 agtgggtgatttttcagaagatcagaagatcaggtgtgataaaatttaaaaaaggctat 1140
 Db 1162 AGTGGTCATTTTACAGATGATGCTGAAGATGACGCTGTGTAATAATTAATAAAGGATT 1221
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 Qy 1201 acagtctactaaattaaagcattaaagaacagataaagaagataag 1249
 Db 1282 TCACATATACACACTTAATAAATAATTAATAAAGATTGAATTGAAGAGG 1330

RESULT 13
 A97496 A97496 Sequence 52 from Patent WO9916780. 1343 bp DNA linear PAT 26-JAN-2000
 DEFINITION
 ACCESSION A97496
 VERSION A97496.1 GI:6780842
 KEYWORDS
 SOURCE Staphylococcus hominis.
 ORGANISM Staphylococcus hominis
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.

REFERENCE
 AUTHORS Gala, J. and Vanuifel, P.
 TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 JOURNAL Patent: WO 9916780-A 52 08-APR-1999;
 GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
 LOCATION/Qualifiers

FEATURES
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 BASE COUNT 544 a 161 c 218 g 420 t
 ORIGIN

Query Match 52.5%; Score 681; DB 6; Length 1343;
 Best Local Similarity 71.6%; Pred. No. 3.7e-107;
 Matches 894; Conservative 0; Mismatches 355; Indels 0; Gaps 0;
 Qy 1 acgagcggtgaatttgggtgcttccagatcaaatgagcagcattccattccacgcaaatg 60
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 Qy 61 gtagggaactgaattaaagggttctgaaagggttgaacacacatcttgcggcattaaa 120
 Db 142 ACTGAAAATTAATAGAGTTAAAGTTCCTGAGAAAACCTGAAACTCATTTAGTAGGAATTA 201
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 Qy 181 tttataatttttttcaaacccgagcagcagcagcagcagcagcagcagcagcagcagcagc 240
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Qy	790	atcgacaagcgctcgaaatcagaagaagccataataaaaaaataatttcagagcaacaa	849
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Qy	850	ctagaagcgaatcaagctcaaaataaaagaagcagaacacttgcacactaaacacggtgac	909
Db	3734	CTCGATGCNAATCAGCAAAAATTAATGAAGCTAAAACTTAAACAAAGAACAATGCCAAT	3793
Qy	910	acattaccgatttcggctggattctttattatttaatccattgaggttggttattatgca	969
Db	3794	GAATTACCATCTCTGCTGGGTCTTTAATTAATCCGTTTGAAGTAGTATTACGCT	3853
Qy	970	ggcggcacagcaacgaatttcgctatttgcgtgaagctacgcagtcgaatgggaatg	1029
Db	3854	GGTGGAACTTCNAATCGTTATCGCCATTTTGCAGGAGCTATGCGGTTCATGAGAAATG	3913
Qy	1030	attaatatgcgattgattatcaaatccaagatataacttttatgcattagtggtgat	1089
Db	3914	ATTAACATATGCAATTGAACATGGTATTAATCACTGGGTATAATTTCTATGGTATTTAGTGGTGAC	3973
Qy	1090	ttttcagaagatgcagcaagctgcagggtgataaaatttaaaaaaggctataatgcagaa	1149
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Qy	1210	ttaaaattaaagcaattaaaaacacagaagataaaaaagataagatatagcaaa	1259
Db	4094	AGAACACTTTAAAAACCTAAAGAAATAGATTTTAAAGAAAGGGAATTATCTAA	4143

Search completed: June 20, 2002, 22:13:00
Job time: 36590 sec

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VERSION		AX145015.1	AX145015.1	VERSION	GI:14283580				
KEYWORDS				KEYWORDS					
SOURCE				SOURCE					
ORGANISM				ORGANISM					
REFERENCE				REFERENCE					
AUTHORS				AUTHORS					
TITLE				TITLE					
JOURNAL				JOURNAL					
FEATURES				FEATURES					
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				Query Match	52.0%; Score 674; DB 6; Length 4434;				
				Best Local Similarity	71.2%; Pred. No. 4.7e-106;				
				Matches 890; Conservative	0; Mismatches 360; Indels 0; Gaps				
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Db	2894	GAATTATTGACTCTTACTGATCGTATGACATATAGTCATTTTACACAAATGGAAGGTAAT	2953						
Qy	70	tatgaattaaaggctgctgaaggcttgaacaacacatctgttcggcattcaagaataacaac	129						
Db	2954	TACGAATTAAAGGTGCTGAAGGTACCGAGTCACATTTAGTTGGAATTAATAATTAATGAT	3013						
Qy	130	aataacgtactagcagcagtttactgacgacgctgcagtaagtgaagttttttaaataat	189						
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Qy	250	tttaatgaactttcaaatatgtttaagaaatatcaagcattatttgaggtagacact	309						
Db	3134	TTTAATGAATTCAGTAAATATGTAATAAAATTAATTTGTTTATATTTAAGNMGTCACCA	3193						
Qy	310	tattaccaaatttaagcgaacacctgatggtgaagtgattgaagatcacgcagtgac	369						
Db	3194	TACCTTCCATATCAATATTTAAATCAAGGGAGAAATACTGGAAATGCAGGTCATGAT	3253						
Qy	370	tggttttttgataaatggctgtaattaaactttgaacatgaaggtttcacactgggttt	429						
Db	3254	TGGATTTTGATCAATTTAGAGAGTTTAGGATATAAACACGAGGATTTCCACAAGGATTT	3313						
Qy	430	gatacaataagcgaacttcgcttttcaattctgtcgtcatgttgaaataaaacatcaaaa	489						
Db	3314	GATCCTGTATTAACAATCCGATATCATCTGTTCTTAATTTACGAACAAGAGTGCTAAT	3373						
Qy	490	gacatcttaatacaaatggataatttaaggaagaagaaatacagcaaaaagtaacagaaaaat	549						
Db	3374	GATGTTTATAAAAACATGGATGGTTTAAAGAAACGGTAAATACTAAAAAAGTTAAGAAAAAT	3433						
Qy	550	ggtgtgaagtcgcgtctatcaaacgaagatgaattacatatatttcctgcgttttatgaa	609						
Db	3434	GGAGTTAAAGTCGGCTTTTATCTCGAAGAAGAGTAGTACCTATATTTAGTGTCATTTATGGG	3493						
Qy	610	gatacatctgaacaaaagattttgtatagatgacgcagtttttatttattcatcogtatg	669						
Db	3494	GATACCTCTGAACACTAAAGATTTTCAGATAGAGAGATAGTCTTTTATTTTACACAGATTC	3553						

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us-09-509-234c-48.rge

Fri Jun 21 08:38:22 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: June 20, 2002, 14:46:22 ; Search time 1139.49 Seconds
(without alignments)
1954.241 Million cell updates/sec

Title: US-09-509-234C-48
Perfect score: 1297
Sequence: 1 acgacggctgaattgggtgc.....tatgaattacagagtaa 1297

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1297	100.0	1297	20 AAX37802	Staphylococcus sch
2	722.6	55.7	1371	20 AAX37805	Staphylococcus sap
3	703.4	54.2	1295	20 AAX37800	Staphylococcus xyl
4	674	52.0	4434	22 AAX54373	S. epidermidis gen
5	672.2	51.8	1342	20 AAX37804	Staphylococcus hom
6	670.6	51.7	1283	20 AAX37801	Staphylococcus cap
7	666.4	51.4	1257	15 AAX78141	Staphylococcus epi
8	652.6	50.3	1305	20 AAX37798	Staphylococcus hae
9	645.6	49.8	1280	20 AAX37799	Staphylococcus lug

10	635	49.0	1179	22 AAX52400	S. epidermidis ope
11	601.6	46.4	1284	20 AAX37803	Staphylococcus sci
12	589.2	45.4	1328	20 AAX37797	Staphylococcus sp.
13	386	29.8	3115	22 AAX53994	S. epidermidis gen
14	322.8	24.9	3821	18 AAX74615	Staphylococcus aur
15	310	23.9	6528	21 AAX49723	Staphylococcus sim
16	282.8	21.8	1470	20 AAX22843	Staphylococcus aur
17	282.8	21.8	1470	20 AAX22843	Staphylococcus aur
18	281.2	21.7	1245	23 AAX55125	Staphylococcus aur
19	280.8	21.6	3271	18 AAX74747	Staphylococcus aur
20	256	19.7	1260	23 AAX54419	Staphylococcus aur
21	254	19.6	1257	23 AAX51636	Staphylococcus aur
22	252.8	19.5	1260	20 AAX07088	Staphylococcus aur
23	252.8	19.5	1260	20 AAX07091	Staphylococcus aur
24	250	19.3	1254	22 AAX52401	S. epidermidis ope
25	234.6	18.1	2453	22 AAX74775	S. epidermidis gen
26	221.8	17.1	453	21 AAX26858	Essential Staphylo
27	221.8	17.1	453	21 AAX26858	Staphylococcus aur
28	221.8	17.1	453	22 AAX08009	Staphylococcus aur
29	221.8	17.1	453	22 AAX08009	Staphylococcus aur
30	206.4	15.9	410	21 AAX26855	Essential Staphylo
31	206.4	15.9	410	22 AAX08006	Staphylococcus aur
32	206.4	15.9	410	22 AAX08006	Staphylococcus aur
33	193.6	14.9	514	18 AAX89751	Synthetic DNA frag
34	185.8	14.3	420	20 AAX26853	Essential Staphylo
35	170	13.1	400	21 AAX26853	Staphylococcus aur
36	170	13.1	400	22 AAX08004	Staphylococcus aur
37	170	13.1	400	22 AAX08004	Staphylococcus aur
38	147.2	11.3	795	23 AAX50908	Staphylococcus aur
39	144	11.1	543	22 AAX71123	C. glutamicum SRT
40	143.6	11.1	1221	18 AAX74940	Staphylococcus aur
41	137.2	10.6	1281	23 AAX52835	Enterococcus faeca
42	127.4	9.8	10194	20 AAX13028	Enterococcus faeca
43	91	7.0	1266	23 AAX54453	Staphylococcus aur
44	90.2	7.0	1263	23 AAX51692	Staphylococcus aur
45	89.6	6.9	289	18 AAX75592	Staphylococcus aur

ALIGNMENTS

RESULT 1
AAX37802
ID AAX37802 standard; DNA; 1297 BP.
XX AC AAX37802;
XX XX 09-JUL-1999 (first entry)
XX XX Staphylococcus schleiferi Fema DNA.
XX DE Staphylococcus schleiferi Fema DNA.
XX KW Fema; identification; detection; therapy; infection; femB;
XX KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX OS Staphylococcus schleiferi.
XX XX Location/Qualifiers
FH Key 1..1297
FT CDS /*tag= a
FT /*product= "Fema"
FT /*note= "partial sequence, no start or stop codon"

PI Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB: AAY08219.
 XX
 XX
 PT New Staphylococcus-specific oligonucleotides
 PS
 XX Claim 23; Fig 10a-b; 48pp; English.
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleotide sequence can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 XX Sequence 1297 BP: 495 A; 184 C; 249 G; 369 T; 0 other;

Query Match 100.0%; Score 1297; DB 20; Length 1297;
 Best Local Similarity 100.0%; Pred. No. 3.6e-255;
 Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 gtggaggaactatgaattaaagtgtgtgaaggtgttgaacaacatttcggaattaa 120
 OY 121 gatacaacaataacgctactagcagcattttacagagaagcgaaggaatgaatt 180
 DB 121 gatacaacaataacgctactagcagcattttacagagaagcgaaggaatgaatt 180
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 DB 301 gtaagaccctatttaccacatgttaagcgaacacatgagtggaagtgaagatac 360
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 DB 361 ggcagtgagcgtgtttttgataaaatgtgctgaattaaacttgaacaggaagttcaca 420
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 DB 481 acatcaaaagacatcttaaatcaatgataatttaagaaaagaatacgaataaagta 540
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 DB 541 cagaanaaatggtgtaaaagtcgctatctaaacgaagatgaattatcttcggttcg 600
 OY 601 ttatcggaagatacatctggaacaaaagattttgagatagatgacattttatat 660
 DB 601 ttatcggaagatacatctggaacaaaagattttgagatagatgacattttatat 660

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 DB 661 catcgtatgaataactataaagatcgtgtccgctacccactagcgtatatttatt 720
 OY 721 gatatttagagagcgtcaaacactgaagcgaagactttaaaaagaattgcgaagca 780
 DB 721 gatatttagagagcgtcaaacactgaagcgaagactttaaaaagaattgcgaagca 780
 OY 781 gataaagacatcgacaagcgtcctgaaatacagaagacccatataaaagaataatta 840
 DB 781 gataaagacatcgacaagcgtcctgaaatacagaagacccatataaaagaataatta 840
 OY 841 gagcaaacacttagaagcgaatcaagctaaataaagaacagaacatltgcaactaaa 900
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 OY 901 caagtgacacatcacccgatttcggtgattccttattatccattgaggttgtt 960
 DB 901 caagtgacacatcacccgatttcggtgattccttattatccattgaggttgtt 960
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 DB 1201 acatctacttaataaataaagaacttaaaagacagaataaaagataagataagcaag 1260
 OY 1261 agaagggatttattgtgtaaaatttcagagttca 1297
 DB 1261 agaagggatttattgtgtaaaatttcagagttca 1297

RESULT 2
 AAX37805
 ID AAX37805 standard; DNA; 1371 BP.
 XX
 AC AAX37805;
 XX 09-JUL-1999 (first entry)
 DT
 XX
 DE Staphylococcus saprophyticus Fema DNA.
 XX
 KW FemA; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Staphylococcus saprophyticus.
 XX
 FT Key Location/Qualifiers
 FT CDS 64..1326
 FT /*tag= a
 FT /product= "FemA"
 XX
 PN W0916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.

[illegible]

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Qy	1213	aaattaaagcaataaagaacaaatgaagaatataagcaagagaagggatatt	1277
Db	1213	acattaaag-----aaattaaagataaagaagaataaacattatagaagggactaa	1268
Qy	1273	attggtatgaatttacagagttaa	1297
Db	1268	gctagaatgaatttacagagttaa	1292

RESULT 4
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 ID AAH54373 standard; DNM; 4434 bp.
 XX
 XX AAH54373:
 AC
 AC
 DX 03-SEP-2001 (first entry)
 DX
 DX
 DE S. epidermidis genomic polynucleotide sequence SPQ ID NO:3737.
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 XX Staphylococcus epidermidis SRI strain; Infection; diagnosis;
 KW vaccination; endocarditis; ds.
 XX
 XX Staphylococcus epidermidis.
 XX

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Dd	514	gaigtctttaaacaacacagatgygttttagaanaagcgtaatactaanaagtcangaanaat	573
Oy	550	ggctgcgaagtcgccgtctccaaacgaagataaattcatatttcgcgttcgtttatygaa	609
Oy	574	ggaglttaagtcgcgccttttatcttcgaagaagatcttcctcattttagtcattatgag	633
Dd	610	gatcacatcgaaacaaagaatttggatagatgagatgcagattttttatatcatogtaig	669
Dd	634	gatacccttgaacctaaaggatttggagatagagaagatagtttttatcaacagagattc	693
Oy	670	aataactataaagatcgygcccgcgcgcacacatagcgtatattgatatttaalcabatta	729
Dd	694	aaacattataaagacccgtygttttagtaaccaacagctcataataacttcgttgatgata	753
Oy	730	ggaaggtctcaacccctgaaagcgcaagactttaaaaaaagaattgcgaagcagataagac	789
Dd	754	gaggaactaataataatgaaagaagaatgctcttaataagattataaagctttaaaagc	813
Oy	790	atcgcaagacgcttcctgaaatcagaaagccataataataaagaaaaatttaggcacaac	849
Dd	814	attggaaagacgtcccgagaaataaanaagacatacaaaaaggaanaatttagacaaca	873
Oy	850	ctagaagcgagatcaagctcaataataaagaagcaganaacattgcacaathaacaacgtgac	909
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ID	AAK37798	standard; DNA; 1305 BP.	
AC	AAK37798:		
DT	09-JUL-1999	(first entry)	
DE	Staphylococcus haemolyticus Fema DNA.		
KX	Fema; identification; detection; therapy; infection; femB.		
KM	amplification; genotyping; gram-positive bacteria; vaccine; ss.		
OS	Staphylococcus haemolyticus.		
XX	Key	Location/Qualifiers	
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FT	/tag= a		
FT	/product= "Fema"		

us-09-509-234c-48.rng

Fri Jun 21 08:38:22 2002

XX HQ916780-A2.
 XX 08-APR-1999.
 XX 28-SEP-1998; 98WO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 XX P-PSDB; AY08215.
 XX New Staphylococcus-specific oligonucleotides
 XX Claim 15; Fig 6a-b; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 XX based on the consensus femA nucleotide sequence which are used to
 XX develop products for the identification, detection and therapy of
 XX infections. The oligonucleotides can be used for the genetic
 XX amplification, the identification and/or quantification of various femA
 XX sequences which are specific to known or unknown Staphylococci species.
 XX Since the femA sequence is similar to the femB sequence, the
 XX oligonucleotides can also be used for the molecular genotyping of femB
 XX genes of different Staphylococci species or other gram-positive bacteria.
 XX The femA nucleic acids can also be used in therapeutic applications.
 XX They can also be used to identify inhibitors, e.g. antibodies or
 XX antisense oligonucleotides, for blocking expression of the femA
 XX nucleotide sequences. They can also be used for producing vaccines
 XX against Staphylococci infections.
 XX Sequence 1305 BP; 513 A; 165 C; 222 G; 405 T; 0 other;
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 XX Query Match 50.3%; Score 652.6; DB 20; Length 1305;
 XX Best Local Similarity 69.3%; Pred. No. 6.5e-124;
 XX Matches 889; Conservative 0; Mismatches 394; Indels 0; Gaps 0;
 XX
 XX 1 acgacggctgaattggtggtttacagatcaaatgacatggttggaacacacatcttgcgcaataa 60
 XX 22 acagtcacagagtttggcaattatcacagataagatgacatggttcacacacaaatg 81
 XX 61 gtagggaactatgaattaaagttgctggaaggttggaacacacatcttgcgcaataa 120
 XX 82 acggaactatgagatgaaggttgcaataaaacagaaactcacttagtgggtataaaa 141
 XX 121 gataacacactaactagctactgagcagctgttactgacagcagtgccagtaagtgatt 180
 XX 142 aataagataatgaggtattgctgacgctgctgacagcagtgacagcagtaagtaatt 201
 XX 181 ttttaataatttttttcaaacggcgacgctgctgacgacgacgacgacgacgacgct 240
 XX 202 ttaagacttttttttcaaacggcgacgctgctgacgacgacgacgacgacgacgct 261
 XX 241 cacttttttttttcaaacgacgacgacgacgacgacgacgacgacgacgacgacgac 300
 XX 262 cacttttttttttcaaacgacgacgacgacgacgacgacgacgacgacgacgacgac 321
 XX 301 gtacacccctatttaccacgacgacgacgacgacgacgacgacgacgacgacgacgac 360
 XX 322 gttgacccctatttaccacgacgacgacgacgacgacgacgacgacgacgacgacgac 381
 XX 361 ggcagtgactggtttttttgataaaatgctgaataaaatgacacgacgacgacgacgac 420
 XX 382 ggtatgattggtttttttgataaaatgctgaataaaatgacacgacgacgacgacgac 441
 XX 421 actgggtttgtacataaaggaattcgttttcttctgtgctgcgattgttgaaataaa 480

Db 442 aaaggttttgatccgattaaacaaatccgatatcatctctgttttagattaaaaataaa 501
 Qy 481 acatcaaaagacatcttaaatcaaatgggataatttaaggaaagaaataacgaaaaagta 540
 Db 502 acatcaaaagacatcttaaatcaaatgggataatttaaggaaagaaataacgaaaaagta 561
 Qy 541 cagaaaaatggtggaagtcgcgtatctaaacgaagatgaattacatattttccgttcg 600
 Db 562 caaaaaatggtggaagtttaagttcttatcagaagaagacttccaattcttcgttca 621
 Qy 601 tttatggaagatacatctgaacaaagattttgataagatagatgacgattttttattat 660
 Db 681 tttatggaagatacatctgaacaaagattttgataagatagatgacgattttttattat 681
 Qy 720 catcgtatgaataactataaagatcgtgctgcggtaccacagcgtatattgtattat 720
 Db 741 aatcgtatgaataactataaagatcgtgctgcggtaccacagcgtatattgtattat 741
 Qy 780 gcatatttagcagctcaacacgtgaagcgcgaagcttttaaaaaagaaattgcaaaagca 780
 Db 801 gcatatttagcagctcaacacgtgaagcgcgaagcttttaaaaaagaaattgcaaaagca 801
 Qy 840 gataagacatcagacagcgtcctgaaatcagaagccataataataaagaaataattta 840
 Db 861 ttaaaagattttgaaacacgacacacaaataaaaggcatttaataaaaaagaaatctt 861
 Qy 900 gagcaacactagagcgaatcaagctcaaaataaaagaagcagaacacattgcaactaaa 900
 Db 921 gaaacacactagagcgaatcaagctcaaaataaaagaagcagaacacattgcaactaaa 921
 Qy 960 caaggtgacacattacagcgttgcgtggtggttctttatttaattcattgaggtgtt 960
 Db 981 caaggtgacacattacagcgttgcgtggtggttctttatttaattcattgaggtgtt 981
 Qy 1020 caaggtgacacattacagcgttgcgtggtggttctttatttaattcattgaggtgtt 1020
 Db 1041 tattatgacgagcgcagacgaagcgaatctgctcattttgtggaagcgcagcagtgcaa 1041
 Qy 1080 tgggaatgatttaattatgagcgttgcgtggtggttctttatttaattcattgaggtgtt 1080
 Db 1101 tgggaatgatttaattatgagcgttgcgtggtggttctttatttaattcattgaggtgtt 1101
 Qy 1140 agtgggtattttcagaagatgcagagatgcagagtggtgataaaaaatttaaaaaaggtcat 1140
 Db 1161 agcgtgtaatttagtgaagcgcgtggaagatggtggaagcatttaaaatttaaaaaaggttc 1161
 Qy 1200 aatgcagaagtaataagatagcgtggtggtggttatttaacgtataaaacacacctgctat 1200
 Db 1221 aatgcagaagtaataagatagcgtggtggtggttatttaacgtataaaacacacctgctat 1221
 Qy 1260 acagtcatttcaaaataaagcaatttaaaagacagataaaaaagataagatatagcaag 1260
 Db 1281 tcagtgtaagaac 1281
 Qy 1282 aatagaaattacagaggttaaa 1304
 Db
 XX RESULT 9
 XX AAX37799
 XX ID AAX37799 standard; DNA; 1280 BP.
 XX AC AAX37799;
 XX 09-JUL-1999 (first entry)
 XX Staphylococcus lugdunensis FemA DNA.
 XX FEM: identification; detection; therapy; infection; femB;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX Staphylococcus lugdunensis.
 OS

```

XX Key Location/Qualifiers
FH CDS 1..1280
FT /tag= a
FT /product= "FemA"
FT /note= "partial sequence, no start or stop codon"
XX
XX MO9916780-AZ.
XX
XX 08-APR-1999.
XX
XX 28-SEP-1998; 98MO-BE00141.
XX
XX 26-SEP-1997; 97EP-0870146.
XX
XX (BENA-) BELGIAN MIN NAT DEFENCE.
XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
XX Gala J, Vannuffel P;
XX
XX WPI; 1999-287521/24.
XX P-PSDB; AAY08216.
XX
XX New Staphylococcus-specific oligonucleotides
XX
XX Claim 17; Fig 7a-b; 48bp; English.
XX
XX This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
XX develop products for the identification, detection and therapy of
XX infections. The oligonucleotides can be used for the genetic
XX amplification, the identification and/or quantification of various femA
XX sequences which are specific to known or unknown Staphylococci species.
XX Since the femA sequence is similar to the femB sequence, the
XX oligonucleotides can also be used for the molecular genotyping of femB
XX genes of different Staphylococci species or other gram-positive bacteria.
XX The femA nucleic acids can also be used in therapeutic applications.
XX They can also be used to identify inhibitors, e.g. antibodies or
XX antisense oligonucleotides, for blocking expression of the femA
XX nucleotide sequences. They can also be used for producing vaccines
XX against Staphylococci infections.
XX
XX Sequence 1280 BP; 484 A; 197 C; 221 G; 378 T; 0 other:

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Query Match 49.83; Score 645.6; DB 20; Length 1280;
Best Local Similarity 70.18; Pred. No. 1.7e-122;
Matches 867; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

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OY 9 tgattgtgtgtgtttacagatcaatgcatatagcatttcaacgaatgttaggaa 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 9 tgattcgggtgtttcacagatcaatgcatatagcatttcaacgaatgttaggaa 68
OY 69 ctatgattaaagtgtctgaaggtgttgaacacatcttgcgcatataagataa 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 69 ctatattttaaagtgtcgaagaaacgaacacatttattgtgtttaaataa 128
OY 129 caataagctactagcagatgttactgacagcagtgccaaatgaagtattttaa 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 129 taacgaagtattgacagatgttattgacagctgtaccacatcgtgtttttaa 188
OY 169 ttattatcaaacgcgcagcagctatgactgaataaagaagctgtcatttct 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 169 cttaacgaataagagccagctatgattgttaacgaacttgaacttttct 248
OY 249 tttaatgaacttcaaatatgttaagaataatccgcatattgttagagtagacc 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 249 cttaatgagctactcaaatattttaaagaataatcgtctcattgtccgcatag 308
OY 309 ttatttcaaatgttaagcgaacatgtagtgtaagtattgaagatacgcagtag 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 309 atacttacttcaataatagagacatgacgtgttaataaagcgaatgtctgca 368

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OY 369 ctgggtttttgataaagtgtgaattaaacttgaacatgaagtttccacactggtt 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 369 ttggttttcaataaagtgaacacactgcgataccatcctatgtgtcttcaacagatt 428
OY 429 tgatacaataagcgaattcgttttcttctgtcgcgagtgttgaataaacaatcaa 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 429 tgatccaatattcaaatgaattccattcttattcttattttaaagtagacagctaa 488
OY 489 agacattatcaaatgataatttaaggaagaataacgaataaagtacaagaaaa 548
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DB 489 agatgttttaataaataatgtagttagttaaagaataaccataaagaatcaaaaa 548
OY 549 tgggtgaaagtcgcctatcctaagagatgataacatttccgttcgtttatga 608
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DB 549 tggagtcgaagtaagttccttaccgaagaagactcctacatttcttcttatttga 608
OY 609 agatacattcaaaaagaatttctgataagatgaatgttttataatcgttat 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 609 gcaagcgtcagaatacctaagaattctctgatagagacgaacatttatacaatcgt 668
OY 669 gaataactataaagatcgtgtcgcgtaccactagcgtatgtattttagatatt 728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 669 taagtactataaagatagtgctgtgtcctcttagcatatttaaaatttagatata 728
OY 729 agcagagctcaacatgaagcgaagactttaaaaagaatgtcaaaagcagataa 788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 729 agagagactcaacgaatgacgaataactttagaaaagatttggcgaagcattaa 788
OY 789 catcgacaagcgtctgaaatcagaagcctaataaagaataaatttaggcagaca 848
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DB 789 catcgagaagcagcagatacaaaaagctataataaagcagaacacttacaacaca 848
OY 849 actagaagcgaatcaagcctaataaagaagcagaacacttacaacacaggtga 908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 849 actcagatgcacatacaaaaagtttaaatgagctatcattgttacaagcagacgt 908
OY 909 cacattacggaattcgtgtatcttattataatcatttgaagttgtttattatgc 968
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DB 909 tggattactatcttgcggtttcttatttattatcgtttgaagttgttatacgc 968
OY 969 agcgcagcagaacgaatcttgcatttttctgtagcagcagctgcattgagaa 1028
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 969 tggagtagcagctaataatctgtcaatttgcaggttagttagcgttctgtaga 1028
OY 1029 gattatttgatgtatttcaatccaatataactttatgttcattagtgtga 1088
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1029 gatttaactatgtatcagacacgcgcataagacagatataatttcaagcattagtga 1088
OY 1089 ttcttcagaagatgagagaatgtaggtgtgtataaatttaaaaagctataatgc 1148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1089 ctcttcagatgagctgtagagcaggtgtcattcgttttaaaaagctatagtcga 1148
OY 1149 agtaataatagtggtgtgttttatttaagcctataaacaacctctatagctta 1208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1149 agtattgaaatagtggtgtgttttatttaagcctataaacaacctctatagctta 1208
OY 1209 cttaaatataagcaatlaaagaacagataaag 1244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1209 ttcaagttaaacgatttcaaaaataagctatagag 1244

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RESULT 10
AAH52400
ID AAH52400 standard; DNA; 1179 BP.
XX
XX AAH52400;
XX
XX 03-SEP-2001 (first entry)
XX
XX S. epidermidis open reading frame nucleotide sequence SEQ ID NO:193.
XX
XX Staphylococcus epidermidis SRI strain; infection: diagnosis;
XX
XX vaccination; endocarditis; ds.
XX

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XX Key Location/Qualifiers
 FH CDS 1..1284
 FT /tag="a"
 FT /product="FemA"
 FT /note="partial sequence, no start or stop codon"
 XX MO9916780-A2.
 PD 08-APR-1999.
 XX 28-SEP-1998; 98MO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 PI WPI: 1999-287521/24.
 DR P-PSDB: AAY08220.
 XX New Staphylococcus-specific oligonucleotides
 PT Claim 25; Fig 11a-b; 48pp; English.
 PS
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococcal species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococcal species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococcal infections.
 CC
 SO Sequence 1284 BP; 518 A; 181 C; 215 G; 370 T; 0 other;

Query Match 46.48; Score 601.6; DB 20; Length 1284;
 Best Local Similarity 67.98; Pred. No. 1.6e-113;
 Matches 874; Conservative 0; Mismatches 404; Indels 10; Gaps 2;

QY 10 gaattggtcgttcacagatcaatgcatatagcatttcacgcaaatgtgaggaac 69
 DB 7 gaattcaagctttcaacaataaagtcgtagcgcatattacaagaagagagtaat 66
 QY 70 tatgaataaaggtcgtcgaaggtgttgaacaacacatctgtgcgcataaagataaac 129
 DB 67 tatgaataaacaacatcgaaggttactcaacacatttgaagggtcgaagataatca 126
 QY 130 aatacgtactagacagcatgttactgacagcgtccagtaagtaagttttaaat 189
 DB 127 ggtgagatattagctgcgtctgttacaagtgtagccagttatgaagaataattac 186
 QY 190 ttatttcaaacgcggaacgtagtactgactacgaaataaagagctggttcctt 249
 DB 187 ttattcaaatagagacaggaatgattatgacacaagaactgttgaacttttc 246
 QY 250 tttaataacttcaaatatgttaagaataatcaccattgattttagagtagacct 309
 DB 247 tttaagaatcgtgagcattttaaagttataaagattatctttagatgcacct 306
 QY 310 tattcaagatgttaagcgaacacatgattgtgaagtttgaagaatcagcagtgac 369
 DB 307 tactgcatacaactaagaagatcatgtgacatatttaaaatcattcaaccgcat 366

QY 370 tggtttttgataaagtcgtaattaaactttgaacatgagaggttcacacactgggtt 429
 DB 367 ggttaattaaacatttgaatcatttagttagcacaacaggtcttcaacactgtttc 426
 QY 430 gatcaataagcgcaatttcgtttcattcgtcgtcgtcgtgaataataaacaatcaaa 489
 DB 427 caccacaatcacatcaatcagatcgtcattcgttactgttactgttaagaagtagcgaag 486
 QY 490 gacattcaataacatggaataatttaagaaagaataacgaaataaagtagcagaataat 549
 DB 487 acgctcacagaacacagacagtttaagaanaagaataaagaattcaaaaatcacaataat 546
 QY 550 ggtggaaggtccgcatctcaaacgaaagatgaattatatttcgttcgtttatgga 609
 DB 547 ggttgaaggtcgtttcctatcattaaagatgaatgccgattatccgcatattatgaa 606
 QY 610 gatacatcgaacaaagaattttagatagatgagatgacgattttattatcactgtatg 669
 DB 607 gatatacagaagaagaagatttcaacgactggtgcgtagatcattcatatagatatta 666
 QY 670 aaatactaaagatcgttcggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 729
 DB 667 aaatacttgaaaa---tgtaagatcctttagatcatatagacttgaacttgaacttacc 723
 QY 730 gcagagctcacactggaagcgaagctttaaagaagaattgcaaaagcagataaagac 789
 DB 724 ccaaatagaaaagaacatgacatgacatcaacaagaagatttgcaaaagctgaaaaagat 783
 QY 790 atcgaagagcgtctgtaanaatcgaagaagccataaataaagaataatttagagaacaa 849
 DB 784 ttgaanaagaacacagatatacaaaaacgatttaataaataagcacttaaaaacaa 843
 QY 850 ctgaagcgaatcaacgctaaataaagaagaagaacatcgtcaacttaaacacgtgtac 909
 DB 844 agagaagcaaatgaagcctaaattgaagaagccttcaacacacagaacatgtgtat 903
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 DB 904 acattaccgaatgcagcgtgttcttattatcaatcattgaggtgtttattatga 963
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 DB 964 ggtgttcacgcgaatgaatatacgtcacttcgcagtgagttatgacatcagtggaatg 1023
 QY 1030 attaatatgcgattatattatcaaatccaaagatataactttatgcatatgtgtat 1089
 DB 1024 attaaacgcgtttagatatacaaatcgttaccgttataactttatgtagcagcgaagac 1083
 QY 1090 ttltcagaagatcagaagatcaggtgtgtatnaaatttaaaaagcgtataatgcagaa 1149
 DB 1084 ttctcagaagatgcacgtatgttgcgttatttaaatcttaaaaaggtttacatgagat 1143
 QY 1150 gtaatagaatattcgtgatttttaagccttaaacaaacgtgcctacagctac 1209
 DB 1144 gttatgaatatattgtgtatttcgttaaaccaatttaaacacgcgtacaaagcatat 1203
 QY 1210 ttaaaatnaagcaatnaaagaacagaataaagaataaagatratgcaagaagagga 1269
 DB 1204 acaacaccaa-----aaaagttatlaaaaataatgatttccagtaagaaggaat 1256
 QY 1270 ttattgttatgaaattttacagattaa 1297
 DB 1257 ttatgaatattgaattttacagattaa 1284

RESULT 12
 AAX37797
 ID AAX37797 standard; DNA: 1328 BP.
 XX
 AC AAX37797;
 XX
 DT 09-JUN-1999 (first entry)
 XX

Fri Jun 21 08:38:22 2002

DE Staphylococcus sp. FemA consensus DNA sequence.
XX FemA: identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
XX
OS Synthetic.
OS Staphylococcus sp.
XX
XX W09916780-A2.
XX
XX 08-APR-1999.
XX 28-SEP-1998; 98WO-BE00141.
XX 26-SEP-1997; 97EP-0870146.
XX (BENA-) BELGIAN MIN NAT DEFENCE.
XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
XX Gala J, Vannuffel P;
XX WPI; 1999-287521/24.
XX
XX New Staphylococcus-specific oligonucleotides
XX
XX Claim 1; Fig 3; 48pp; English.
XX This invention describes novel staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
XX develop products for the identification, detection and therapy of
XX infections. The oligonucleotides can be used for the genetic
XX amplification, the identification and/or quantification of various femA
XX sequences which are specific to known or unknown Staphylococci species.
XX Since the femA sequence is similar to the femB sequence, the
XX oligonucleotides can also be used for the molecular genotyping of femB
XX genes of different Staphylococci species or other gram-positive bacteria.
XX The femA nucleic acids can also be used in therapeutic applications.
XX They can also be used to identify inhibitors, e.g. antibodies or
XX antisense oligonucleotides, for blocking expression of the femA
XX nucleotide sequences. They can also be used for producing vaccines
XX against Staphylococci infections. This sequence represents a femA
XX consensus DNA sequence composed from Staphylococcus sp. sequences.
XX
XX Sequence 1328 BP; 304 A; 78 C; 146 G; 227 T; 573 other;
SQ

Query Match 45.4%; Score 589.2; DB 20; Length 1328;
Best Local Similarity 50.5%; Pred. No. 5.4e-111;
Matches 655; Conservative 0; Mismatches 636; Indels 6; Gaps 1;

Qy 1 acgagcggtgaattggtggtttacagatcaaatgcccataagcatttcacgcaaatg 60
Db 35 acngnanagantnnnnntcngannnnatnncnannagcatttnacncanann 94
Qy 61 gtagggaactatgaattgaagggtgtgtgaacacacattgtgcgacattaa 120
Db 95 nnnngnnantngannnttgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 154
Qy 121 gatacaacaatacgtactagcagcatttactgacagcagtcgacgtaagattt 180
Db 155 aanaannataangnangnttgcngcngntnnnnnnnnnnnnnnnnnnnnnnnn 214
Qy 181 tttaataatttttataaaccgagcagcagtcgacgacgataaataagagctgtt 240
Db 215 tnaaantattttatcnaannngngcngcngntatnngattnnanaannagcngtn 274
Qy 241 cattctcttttttaagaacttcaataatgttaagaaataatcacgcattgttggaga 300
Db 275 cantnntctttaangantnnnaantatnnaannnnnnnnnnnnnnnnnnnnnn 334
Qy 301 gtgagacctatttaccatgttaagcggaacacacatgatgtgaagtgattgaagatac 360
Db 335 ntnganocctannntnctatcaatannnnnaatcatgngngannnnnnnnnaatgcn 394

Qy 361 ggcagtgactggttttttgataaaatggctgaattaaacttgaaacatgaaggtttcaca 420
Db 395 ggnnangattggtntngatnannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 454
Qy 421 actggtgttgatacaataaaggcaaatcgttttcatctgtgctgcgtgtaaaataaa 480
Db 455 amngnttgancnntnnnncaatnngntnncantcngntnannatctannnnnnnaaa 514
Qy 481 acatcaaaaagacatcttaataatgaataaattaaaggaagaaatacgaagaaagta 540
Db 515 annncnnanganntnnnaannnnatggtngntnngannngnaannnaacnaaaagtn 574
Qy 541 cagaaaaatggtgaaagtcgcgtctatcaacgaagatgaattacattatttcctgtcg 600
Db 575 nanaanaatgngtnaaagtcnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 634
Qy 601 tttaaggagatcacatctgaacaaagaattttgtatagatagacgagattttattat 660
Db 635 ttnatggatgatacnnncnngannnnaangntnnnnngatnngngannnnnnnnnnnnnn 694
Qy 661 catcgtatgaataactataaagatcgtccgcgtaccactagcgtatattgatttaatt 720
Db 695 aanngtntnnnnnnattnnaaagannnnngtcnngtcnntngntatnntnnttngat 754
Qy 721 gcatattagcagctcaacactgaagcgaagactttaaaaaaagaaataatgcagaaagca 780
Db 755 gantnnnnnnngann 814
Qy 781 gataaagacatcgacacgctcctgaaatacgaagcgcataataaaagaaataatta 840
Db 815 ntnaanganatnganaaangcncnganaanaaaagcngnnnnnnnnnnnnnnnnnnnnnn 874
Qy 841 gagcaacactagaagcgaatacaagctaaataaaagaagcagaaacattgcgaactaaa 900
Db 875 naanacaantnnngcnaannnnnaaaaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 934
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Db 1055 tggnnnatgataaantatgcnntnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1114
Qy 1081 agtgggtattttcagaagatgcagaaatgcaggtgctgataaaatttaaaaggctat 1140
Db 1115 agnggtntantnnangngangcgaagatgngngntnnnnnnnnnnnnnnnnnnnnnnnn 1174
Qy 1141 aatgcagaagtaataatgtcgtgattttatttaagcctataaacaacacgtgcctat 1200
Db 1175 natgngannntnngantngtggnganttnntnaaacnnaatnaaannnnnnnnnnnnnn 1234
Qy 1201 acagtctacttaataaagcaatcaaaagcaagataaaagataagataagcaag 1260
Db 1235 nnn 1288
Qy 1261 agaaggggtatttattggtgataaatttacagagattaa 1297
Db 1289 nann 1325

RESULT 13
AAH53994/c
ID AAH53994 standard; DNA; 3115 BP.
XX
XX AAH53994;
XX
XX 03-SEP-2001 (first entry)
DT

Fri Jun 21 08:38:22 2002

Rosen CA;
XX WPI; 1997-374922/35.
XX polynucleotide(s) and proteins derived from *Staphylococcus aureus*
XX stored on computer readable medium and used in the production of
XX anti-S.aureus vaccines
XX
XX Claim 1; Page 1139-1141; 3271pp; English.
XX This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences
XX of the invention. The DNA sequences are recorded on a computer readable
XX medium, preferably selected from a floppy or hard disk, random access
XX memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
XX the S.aureus DNA sequences allows putative functions to be assigned so
XX that protein-encoding or regulatory regions of commercial, therapeutic or
XX industrial importance can be obtained. Specifically, sequences which are
XX likely to encode antigens have been identified and these polypeptides can
XX be used in a vaccine composition against *S.aureus* infection. The
XX polypeptides can also be used in a kit for the immunodetection of
XX *S.aureus* in a sample. *S.aureus* is implicated in numerous human diseases,
XX including cellulitis, eyelid infections, food poisoning, osteomyelitis,
XX skin and surgical wound infections, scalded skin syndrome, toxic shock
XX syndrome, etc. Organisms transformed with the DNA sequences can be used
XX for recombinant production of the polypeptides. The new DNA sequences
XX (and their fragments) are useful as primers or probes for isolating
XX homologues of any of the *S.aureus* DNA sequences contained on the
XX computer readable medium.
XX
XX Sequence 3821 BP; 1233 A; 548 C; 673 G; 1245 T; 122 other;
SQ

Query Match 24.9%; Score 322.8; DB 18; Length 3821;
Best Local Similarity 52.5%; Pred. No. 1.2e-56;
Matches 624; Conservative 1; Mismatches 563; Indels 0; Gaps 0;

QY 36 gccatattgcccatttcacgcaaatgtaggggaactgaattaaaggttgcgtgaagtggt 95
DB 3820 GCATTTTCACATTACACACAAATCAGCTATTCTTACACATAGAGTTGATTTAAAGG 3761

QY 96 tgaacacattctgtcgccattaaagataaacacaaataagctactgagcgatgttact 155
DB 3760 CGATGTCATCTGTAGGGGTTAAAGATGCAATGCTCAAGTGTTCAGGATGCTGTTATT 3701

QY 156 gacagcagtcgcccgaatgaagttttttaaattttttttaaattttttaaattttttaaattttt 215
DB 3700 GACAGAGCAGCAGCACACTTAAATTTTCAAAATATTTTATACATCGCGGCCAGTGAT 3641

QY 216 ggactaagaaataaagaagctgcttcatttttttttttttttttttttttttttttttttttttt 275
DB 3640 GGATTTATACAAATCATCATATTAGTAGCATTTTCTTTAAAGCATTAACGTCATATTAA 3581

QY 276 gaaatcacgcattgtatttgagagtagaagcatttttttttttttttttttttttttttttttt 335
DB 3580 GAAACACAAATGTTTATGCTCTGTTAGATCCATATTAAATGAAATTTACGCAATGC 3521

QY 336 tgatgggaagtgatgaagatacgcagtgactggttttttttttttttttttttttttttttttt 395
DB 3520 AGACGGTGAATTTGTTAAATCTTATGATTAACCGAGCATTTGTTAGAACAAATGGATAA 3461

QY 396 aaactttgacatgaagtttttcaactgggttttgatacataaaggcaaatcttttca 455
DB 3460 AGTTTATAACACACACAGGTTTCCCTGTAGTTTATGATCAATGAGCAATCCGTTGGCT 3401

QY 456 ttctgtgctgcgtgttgaataaataaacaacataacatacttaataacaaatgataattt 515
DB 3400 GTCACTGTTAGATTAAAGATAAGACTGAAGACCACTTTTAAAGAAATGGATTATCA 3341

QY 516 aaggaataaagaatacagaataagcacagaataatggttgtaagtcgcgtatcttaacga 575
DB 3340 AACGAGACGTAATTTAAATAAACATATGATTTGTTGTCATAAACTAAACAGTTAACGAT 3281

QY 576 agatgaattacattttccgttgcgttttatggaagatacatctgaacaaagaatttgt 635

Db 3280 TGATGAACGCAAACTTTTTCGACTTATTCATATGCTGAGGAAGACGCGTTTCAA 3221
QY 636 agatagatgacgattttttattatcatcgtatgaataactataaagatcgtccgcgt 695
Db 3220 ATTCCGTGAGTTACATACATCTTTGAAGAATGCAAAAGTTTATAGATGACCGACGCTGTT 3161
QY 696 acaactagctatattgatttttaattgcatatttagcagagctcaacactgaagcgcaaga 755
Db 3160 AAAAGTTGGCGTATATTGATTTAAACGAGTATTAAACACGTTTAAATTAAGCAACACACA 3101
QY 756 ctttaaaaaaagaattgcaaaagcagataaaacacacgacgaagcctcctgaaatccagaa 815
Db 3100 ATTAACAGCTGAACCTCTCAGGTGTTGAAGAAGCATTTGAAGAAGTCTTAAATTCAGAA 3041
QY 816 agccataataaagaagaatttagcgaacaaactagaagcgaatcaagctcaaaataaa 875
Db 3040 AAATAAAACGAAACGACACACAGCTAGAACACAGCTAAATAGCAATAAGCGTAAATCGA 2981
QY 876 agaagcagaacacattgcaacttaaacacggtgacacattaccgatttcggtggttatt 935
Db 2980 CAATACATAGAACAAATTTGAACAAGATGTCGAGCTTTAAACCTTAGCTTCTGCTTATT 2921
QY 936 tattataatccatttgaggtttgtttattatgcagggcgacagcaaacgaattcgtca 995
Db 2920 TATCTACAATGAGCATGAAGTTTATTCTTATCTAGTGTTCAAACCCCTAAATATATGC 2861
QY 996 ttttgcgtgaagctacgcagtcgaatgggaatgatttaattgattgattgattatcaat 1055
Db 2860 TTATATGGGTCCTACCATTTGTCAGTGGGAATGATTAAGTTTGTCTAAAGCGCATCAT 2801
QY 1056 tccaaagataacattttatggtggtggttttttttttttttttttttttttttttttttt 1115
Db 2800 TGATCGCTATATTTTATGTTTATGCTATTACCGGTGACTTTTCAGATCATCAGAGACTATGG 2741
QY 1116 tgtgataaatttttaaaagcgtataatgcagaagtaagataatgctggtggtttttat 1175
Db 2740 CGTCCAAACAATTTCAAAAAGGTTTAAACGCACATGTAGAANNNNNNNNNNNNNNNN 2681
QY 1176 taagcctataaacaacacctgctatacagctctacttacttaaaattaaagca 1223
Db 2680 NNN 2633

RESULT 15
AA249723
ID AA249723 standard; DNA; 6528 BP.
XX AC AA249723;
XX 18-APR-2000 (first entry)
XX *Staphylococcus simulans* lysostaphin gene allelic variant-3.
XX Lysostaphin; antibiotic; anti-staphylococcal; endopeptidase;
XX gene therapy; mastitis; staphylococcal infection; ruminant; cow;
XX transgenic animal; allelic variant; altered lysostaphin gene; ds.
XX *Staphylococcus simulans*.
XX Location/Qualifiers
XX complement (2329..3810)
XX /tag= a
XX /product= "Lysostaphin"
XX /trans_except= (pos:3808..3810, aa:Met)
XX WO9967381-A1.
XX 29-DEC-1999.
XX 22-JUN-1999; 99WO-US14073.
XX 22-JUN-1998; 98US-0090175.
PR

us-09-509-234c-48.rng

Fri Jun 21 08:38:22 2002

us-09-509-234c-48.rni

Fri Jun 21 08:38:23 2002

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Query Match      17.1%; Score 221.8; DB 3; Length 453;
Best Local Similarity 66.7%; Pred. No. 6.9e-44;
Matches 301; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-9

Query Match      17.1%; Score 221.8; DB 4; Length 453;
Best Local Similarity 66.7%; Pred. No. 6.9e-44;
Matches 301; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

668 tgaatactataaagatcggtccgcgtaccactagcgtatattgatttgaatgcatt 727
3 TAAATATATACAAAGCGGTGTTAGTACCTTTCCTTATATACATCACTTATGAATATA 62
728 tagcagagctcaactgaagcgcgaagcctttaaagaagaattgcaaaagcagataaag 787
63 TTAAGAACTAAACGAGCGGTGATTTTAAATAAAGATTTAAATAAAGCGTTAAAGG 122
788 acatgcagacgctccctgaaatcagaagcgcataataaagaagaatttagagcaac 847
123 ATATTGAAAACGCTCTGAAATATAAAGACGACATACACGCGAGATACCTTACACAAAC 182
848 aactagaagcgaatcaagctaaataaagaagcagaacattgcaacttaaacacggtg 907
183 AACTTGATCAATAGCAAGCGGTGATTTTAAATAAAGATTTAAATAAAGCGTTAAAGG 242
908 acattaccgatttcggtgattttatttatttatttatttatttatttatttatttattg 967
243 ATGNTTACCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302
968 cagcgccagcagcaaaatttccttcatttcttcatttcttcatttcttcatttcttcatt 1027
303 CTGGTGATCAATCAATGCNTCCGTCATTTTCCGANGTATGCTGATGCTGATGCTGATG 362
1028 tgataattatgcgattgattatcaaatccaaagataaacttttattggtcattggtggtg 1087
363 TGNTTATTTTTCATTAATCAATGCGATTTGCCGTTATGCTGATGCTGATGCTGATG 422
1088 attttcagaagatgcagaagatgcaggtg 1118
423 AATTTCNAGNAGTGTCTGAAGATGCTGTGT 453

RESULT 4
US-09-265-315-9
; Sequence 9, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES

Query Match      17.1%; Score 221.8; DB 3; Length 453;
Best Local Similarity 66.7%; Pred. No. 6.9e-44;
Matches 301; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

668 tgaatactataaagatcggtccgcgtaccactagcgtatattgatttgaatgcatt 727
3 TAAATATATACAAAGCGGTGTTAGTACCTTTCCTTATATACATCACTTATGAATATA 62
728 tagcagagctcaactgaagcgcgaagcctttaaagaagaattgcaaaagcagataaag 787
63 TTAAGAACTAAACGAGCGGTGATTTTAAATAAAGATTTAAATAAAGCGTTAAAGG 122
788 acatgcagacgctccctgaaatcagaagcgcataataaagaagaatttagagcaac 847
123 ATATTGAAAACGCTCTGAAATATAAAGACGACATACACGCGAGATACCTTACACAAAC 182
848 aactagaagcgaatcaagctaaataaagaagcagaacattgcaacttaaacacggtg 907
183 AACTTGATCAATAGCAAGCGGTGATTTTAAATAAAGATTTAAATAAAGCGTTAAAGG 242
908 acattaccgatttcggtgattttatttatttatttatttatttatttatttattg 967
243 ATGNTTACCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302
968 cagcgccagcagcaaaatttccttcatttcttcatttcttcatttcttcatttcttcatt 1027
303 CTGGTGATCAATCAATGCNTCCGTCATTTTCCGANGTATGCTGATGCTGATGCTGATG 362
1028 tgataattatgcgattgattatcaaatccaaagataaacttttattggtcattggtggtg 1087
363 TGNTTATTTTTCATTAATCAATGCGATTTGCCGTTATGCTGATGCTGATGCTGATG 422
1088 attttcagaagatgcagaagatgcaggtg 1118
423 AATTTCNAGNAGTGTCTGAAGATGCTGTGT 453

RESULT 3
US-09-265-315-9
; Sequence 9, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon 5 Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: word perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918

```

NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Maiburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-9

Query Match 17.1%; Score 221.8; DB 4; Length 453;
 Best Local Similarity 66.7%; Pred. No. 6.9e-44;
 Matches 301; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

668 tgaataactataaagatcggtcgcgtacacagctatattgatttaacatatt 727
 3 TAAATAATTACAAAGACCGGTGTGATGCTTAAAGCTATATCACTTATATGATA 62
 728 tagcagaagctcaacacgtgaagcgaagactttaaaaaagaattgcaaaagcagtaag 787
 63 TTAATAAATAAGAGAGAGCGATATTATTAATAAAGATTAAATAAGCGTTAAAGG 122
 788 acatcgcaagcgtctcgtgaataacacagcacaataataaaaaagaatttaagagcaac 847
 123 ATATGAAAAAGCTCTGTAATAAAGACACATACAGCGAGATTAACCTTACAAAC 182
 848 aactagaagcgaatcaagcctaataaagaagcagaacacttgcacacttaacacagctg 907
 183 AACTGATGCAAAATGAGCAAAAGATTGANGAGGTAAAGCTGACAAANGANGANGATGTA 242
 908 acacattaccgaattcggtcggtgattcttattattatccatttgaggtgtttatttg 967
 243 ATGTTTACCTATCTCTCTGTTTCCCTTATCAATCCNTTGGAGTTGTTTATVWG 302
 968 cagcgcgacacgaagaatttgcatttgcctggaagcgaacgagcagtcagtcagga 1027
 303 CTGCTGATCAATCAAAATGCTTCCGTATTTTCCGANGTATGCGAGTCAATGGGAAA 362
 1028 tgataattatcgattgattatcaaatccagaatlaaactttatgcatatggtg 1087

DB 363 TGNATATTGCTTAATATCATGCGATTGNCCTTATATTCATGCTGTAGTGATN 422
 OY 1088 atttcagaagatgcagaagatgcaggtgt 1118
 DB 423 AATTTCAGNAGGTGCGAAGATGCTGCTGT 453

RESULT 5
 US-09-266-417-9
 Sequence 9, Application US/09266417
 Patent No. 6228588
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongyu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STRAPHYLOCCUS ADREUS
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/266,417
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Maiburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/248
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-266-417-9

Query Match 17.1%; Score 221.8; DB 4; Length 453;
 Best Local Similarity 66.7%; Pred. No. 6.9e-44;
 Matches 301; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
 OY 668 tgaataactataaagatcggtcgcgtacacagctatattgatttaacatatt 727
 DB 3 TAAATAATTACAAAGACCGGTGTGATGCTTAAAGCTATATCACTTATATGATA 62
 OY 728 tagcagaagctcaacacgtgaagcgaagactttaaaaaagaattgcaaaagcagtaag 787

us-09-509-234c-48.ini

Fri Jun 21 08:38:23 2002

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-6

Query Match 15.9% Score 206.4; DB 3; Length 410;

Best Local Similarity 68.6%; Pred. No. 2.9e-40;
Matches 279; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Db 63 TTAAGACTAAACGAGCGGTATATTTAAATAAGATTAAATAAGCGTTAAAGG 122
Qy 788 acatgcacagcgtccctgaatacagaagccataaaataaaagaaatttagagcaac 847
Db 123 ATATTGAAAAACGCTCGAATAATAAAGGACATACAGAGCGAGATAACTTACAACAC 182
Qy 848 aactgaagcaaatcaagctcaataaaagaagcagaacacattgaacttaaacacgtg 907
Db 183 AACTGATCAAAAGACAAAGATTGANGACGGTAAACGCTTACAAAGANGANCAATGGTA 242
Qy 908 acacattaccgattccgctggtttcttattattattattattattattattattatt 967
Db 243 ATGNTTAACTATCTCTCTGCTGCTTCTCTTATCAATCCNTTGGANGTGTATTATG 302
Qy 968 caggcgacagcaaacgaatttcgctcatttgcgtggaagcagcagcgaatgggaaa 1027
Db 303 CTGGTGATACAAATGCNTCCGTCATTTCNCCGGANGTATGCGTGAATGGGAAA 362
Qy 1028 tgattattatgcgattgattattcaaatcccaagataataacttttgcgattagtggtg 1087
Db 363 TGTATATTTGCAATTAATCATGCGATTGNCGGTTATAATNCTATGCTGTTAGTGTN 422
Qy 1088 attttcagaagatgcagaagatgcaggtgt 1118
Db 423 AATTNCAGNAGGTGCTGAAGATGCTGCTGT 453

RESULT 7

US-09-265-315-6

; Sequence 6, Application US/09265315
; Patent No. 6187541

GENERAL INFORMATION:

APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu

TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

FILED DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-6

Query Match 15.9%; Score 206.4; DB 4; Length 410;
Best Local Similarity 68.6%; Pred. No. 2.9e-40;
Matches 279; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 644 atgacgattttatattatcgttgatgaataatcgtgtccggtacacag 703
DB 4 ATGCAAAATTAACATCAATCGCTTAATAATTAACAAAGACCGTGTGNGTACCTTTAG 63
QY 704 cgtatattgatttaagcatatttagcagagctcaacatgaagcgcaagactttaaa 763
DB 64 CGTATATCACTTTATATGATATTAATAAGACTAAACGAAGCGGTATTTTAAATA 123
QY 764 aagaatttcaaaagagataagacatcgacacgctctctgaaatcagaagccataa 823
DB 124 AAGATTTAATTAAGCGTTAAAGATTAATAAAGCTCTGAATAATTAATAAGCACATA 183
QY 824 ataaagaagaatttagagcaacactagaagcgaatcaagctaaataaagaagcag 883
DB 184 ACAAGCAATTAACATTAACAACAACTGATGCAATGCAAAAGATTGAAGAAGTA 243
QY 884 aaacattgcaacttaaacacggtgacacattaccgatttcggctggattcttattata 943
DB 244 AACGCTACAAAGANGAACAATGATATGAATTAATCTCTCTGTTCTNCTTATCA 303
QY 944 atccattgaggtttattatgagcagcgcaacgaagaatttcgatttggctg 1003
DB 304 ATCCATTGANGTTGTTTATTTGCTGCTGCTGATCAAAATGATCCGATTTTNCGG 363
QY 1004 gaagtaacgagtcgaatgggaatgatttaattcgattgattat 1050
DB 364 GAAGTTATCAAGCAATGGAATGATTAATTAATGATTAATCAT 410

RESULT 8
US-09-265-315-6
Sequence 6, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Yang J.
APPLICANT: Maloun, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STRAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-6

Query Match 15.9%; Score 206.4; DB 4; Length 410;
Best Local Similarity 68.6%; Pred. No. 2.9e-40;
Matches 279; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 644 atgacgattttatattatcgttgatgaataatcgtgtccggtacacag 703
DB 4 ATGCAAAATTAACATCAATCGCTTAATAATTAACAAAGACCGTGTGNGTACCTTTAG 63
QY 704 cgtatattgatttaagcatatttagcagagctcaacatgaagcgcaagactttaaa 763
DB 64 CGTATATCACTTTATATGATATTAATAAGACTAAACGAAGCGGTATTTTAAATA 123
QY 764 aagaatttcaaaagagataagacatcgacacgctctctgaaatcagaagccataa 823
DB 124 AAGATTTAATTAAGCGTTAAAGATTAATAAAGCTCTGAATAATTAATAAGCACATA 183
QY 824 ataaagaagaatttagagcaacactagaagcgaatcaagctaaataaagaagcag 883
DB 184 ACAAGCAATTAACATTAACAACAACTGATGCAATGCAAAAGATTGAAGAAGTA 243
QY 884 aaacattgcaacttaaacacggtgacacattaccgatttcggctggattcttattata 943
DB 244 AACGCTACAAAGANGAACAATGATATGAATTAATCTCTCTGTTCTNCTTATCA 303
QY 944 atccattgaggtttattatgagcagcgcaacgaagaatttcgatttggctg 1003
DB 304 ATCCATTGANGTTGTTTATTTGCTGCTGCTGATCAAAATGATCCGATTTTNCGG 363
QY 1004 gaagtaacgagtcgaatgggaatgatttaattcgattgattat 1050
DB 364 GAAGTTATCAAGCAATGGAATGATTAATTAATGATTAATCAT 410

[illegible]

RESULT 10
 US-08-714-918-4/C
 ; Sequence 4, Application US/08714918
 ; Patent No. 6037123
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Ving Francois
 ; APPLICANT: Malouin, Patrick K.
 ; APPLICANT: Martin, Patrick B.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 ; TITLE OF INVENTION: TARGET GENES
 ; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California

-----TGGGAGGTTCCATTAAATCAT 410

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RESULT          9
US-09-266-417-6
; Sequence 6, Application US/09266417
; Patent No. 622588
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,417
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 240/248
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
ns-09-266-417-6

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	Query Match	15.9%	Score 206.4;	DB 4;	Length 410;
	Best Local Similarity	68.6%;	Pred. No. 2.9e-40;		
	Matches 279; Conservative	0;	Mismatches 128;	Indels	Gaps 0;
644	atgacgatgttttattcatcctgatgaatactataagaatcgctgccgcgtcaccaactag	703			
oy					
Ob	4 ATGCAATNTAACTACAATCGCTTAATAATTACAAAGCCGTGTGNAGTACTTTAG	63			
704	cgtatattgatttttaatgcattatttagcagagctcaacactgaagcgaagactttaaaa	763			
oy					
64	CGTATATCAACTTTTAAATATATTAAAGAACTTAACGGAGAGCGTGATATTTTAAATA	123			
Ddb					
Oy	764 aaagaattqcaaaqcacataaacaacatccacaaagcgcttcctgaaatcggagaagcctaa	823			

Page 8

US-09-265-315-4

Matches 259; Conservativ

280 ATACTGATCATGATGG

Db 40 ATTATTATCTGAAGGAG

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us-09-509-234c-48.rni

Fri Jun 21 08:38:23 2002

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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-4

Query Match      13.1%; Score 170; DB 4; Length 400;
Best Local Similarity 64.8%; Pred. No. 1.1e-31;
Matches 259; Conservative 0; Mismatches 140; Indels 1; Gaps 1;

QY 205 ggacgcacgtatgactgaacataaagagctgttcattcttttttaatagaactt-c 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 GGTCCAGTGATGANTATGAAATCAAGNACTCGTACACTTTTNCCTTAATGAATATCC 341

QY 264 aaatattgaagaataatcagcattgtattgagagtagacccttatttaccatgtt 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 340 AAAATATGTTAAAAACATCGTGTGNCATATACCTACATANGCATCATATTTACCATATCA 281
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 aaagcgaacacatgattggaagtgattgaaagatagcggcagtgactgggttttgataa 383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 ATACTTGATCATGATGGGAGATACAGGTAATGCTGTAATGATGATGATGATGATGATGAT 221
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 aatggctgaattaaactttgaacatgaaggtttcacactgggttttgatacaataagga 443
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QY 220 AATGAGTAACCTAGGATTTGAACATACCTGGAATTCATTAAGGATTTGATCTGTGCTACA 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 444 aatcggttttctctgtgctgctgattgaaataaataacatacaataaagacatcttaataca 503
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US-09-266-417-4

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RESULT 13
 US-09-266-417-4/c
 ; Sequence 4, Application US/09266417
 ; Patent No., 6226588
 ; GENERAL INFORMATION

Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Vling J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
ADDRESS: 633 West 47th Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2086
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918

us-09-509-234c-48.rni

Fri Jun 21 08:38:23 2002

FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5253 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 us-09-265-315-19

Query Match 6.8%; Score 87.8; DB 4; Length 5253;
 Best Local Similarity 49.2%; Pred. No. 6.9e-12;
 Matches 284; Conservative 1; Mismatches 288; Indels 4; Gaps 2;

QY	701	tagctattgatttaattgcatatttagcagagctcaacactgaagcgcaagacttta	760
DB	2636	TAGTAAGTTGGATCCCAAGAAATATAGCGAAAGTAATCAAGATTGAATGAATTC	2577
QY	761	aaaaagaattgcgaagcagataaagacatcgacaagcgt---cctgaaatcagaag	817
DB	2576	ATCCGGAATTCCTAAATGGCAGCAGAGATGAAGATGAAGATTTAAACGAG	2517
QY	818	ccataataaaaaaatttagagcaacaactagaagcggaatcaagctaaaaaag	877
DB	2516	CGCAAAATATGATTAAATGCGCAAAATAAATTTCTFAAATGAAGATTTAAACGAG	2457
QY	878	aagcagaacattgcaacttaaacacggtgacacattaccgatttggtgattctta	937
DB	2456	ACCTAGAGCTTTAGAAAAGGACATCCTGAAGGTATTATCTTTCTGTGACATTTAA	2397
QY	938	ttattaatcatttgaggtgtttattatgcagcgccgacagcaaacgaatttcgtcatt	997
DB	2396	TGTTTGTGGCTCAAAATCATATTACTTATATGGTGGCTCTCTAATGAATTTAGAGATT	2337
QY	998	ttgctgaagctacgcagtgcaatgggaatggaatattgaattgagatttatcaaatc	1057
DB	2336	TTTTACCAATCATCATATGTCAGTATACGATGATGAAGTATGACGTCAGTGAACATGGTGCA	2277
QY	1058	caagatataacttttagcattagtggtgattttcagaagatgcagaagatgcaggtg	1117
DB	2276	CAACTTACGATTTCGGTGCAGATAATGATCCAGATTAACACTCAGACATTATGGAT	2217
QY	1118	tgataaaatttaaaaggctataatgcagaagtaataagaatagattgctggtgatttt-att	1176
DB	2216	TATGGGCATTTAAAAAAGTGTGGGACATACTTAAGTGAAGATTTGGTGAATTTGATT	2157
QY	1177	aagcctataaaacacctgctatacagtcacttaaaattaaagcaattaaagacaag	1236
DB	2156	ATGTATTGAATCAGCCATTGTRCAATTAATTGAGCAAGTTAAACCGCTTTACAAAG	2097
QY	1237	ataaaagaatagatatagcaagaagaggggattta	1273
DB	2096	CTAAATTAATAATCTCGTAATTAACGGAATA	2060

Search completed: June 20, 2002, 12:04:07
 Job time: 20962 sec

Fri Jun 21 08:38:25 2002

us-09-509-234c-48.rst

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:26:50 ; Search time 8551.36 Seconds
(without alignments)
2047.107 Million cell updates/sec

Title: US-09-509-234C-48
Perfect score: 1297
Sequence: 1 acgacgcgcgaattcgtgc.....tatgaattacagagttaa 1297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
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8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	77.6	6.0	1135	12	CNS0336Q
2	76.8	5.9	1101	12	CNS0021J
3	75.2	5.8	885	12	AG136199
4	75	5.8	614	12	CNS0152H
5	74.8	5.8	619	9	AL514935
6	73	5.6	652	12	CNS03H0U
7	72	5.6	907	12	CNS02134
8	71.8	5.5	894	12	CNS018BG
9	71.4	5.5	879	12	CNS00601
10	71.4	5.5	910	12	BM415636
11	71.4	5.5	834	12	B12387
12	71	5.5	1101	12	CNS0039G
13	70.8	5.5	966	10	BM415686
14	70.2	5.4	1036	12	CNS00599
15	69.6	5.4	660	12	BH183498
16	69.6	5.4	660	12	CNS070NT
17	69.6	5.4	660	12	CNS070NT

18	69.4	5.4	756	3	B1644558
19	68.2	5.3	974	12	CNS0017T
20	69.2	5.3	1101	12	CNS001PB
21	69	5.3	1101	12	CNS01772
22	68.6	5.3	905	12	A2550256
23	68	5.2	1247	12	B13042
24	67.8	5.2	922	12	A2548363
25	67.8	5.2	1007	12	CNS06X9S
26	67.8	5.2	1101	12	CNS00GPB
27	67.2	5.2	865	12	A0324474
28	67	5.2	788	12	A2195503
29	67	5.2	769	12	AG134867
30	67	5.2	1001	12	CNS01400
31	66.8	5.2	483	12	CNS02CV8
32	66.8	5.2	802	12	CNS01772
33	66.6	5.2	1223	12	B12981
34	66.6	5.1	833	12	A0446640
35	66.6	5.1	838	12	A2199419
36	66.6	5.1	1101	12	A2199419
37	66.4	5.1	581	12	CNS00KHB
38	66.4	5.1	1092	12	CNS020K7
39	66.2	5.1	850	12	A2186328
40	66.2	5.1	1101	12	CNS00H87
41	66	5.1	770	12	A2196926
42	66	5.1	1101	12	CNS0153V
43	66	5.1	1139	12	A0897537
44	66	5.1	1184	12	B13117
45	65.6	5.1	908	12	AG160668

ALIGNMENTS

RESULT 1
CNS0336Q 1135 bp DNA linear GSS 15-MAY-2000
LOCUS Tetradon nigraviridis genome survey sequence POC-ori end of clone
DEFINITION 208P24 Of library G from Tetradon nigraviridis, genomic survey sequence.

ACCESSION AL226115
VERSION AL226115.1 GI:7885026
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nigraviridis.
ORGANISM Tetradon nigraviridis.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Fitzames C., Fisher C.,

REFERENCE 2 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 3 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 4 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 5 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 6 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 7 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 8 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 9 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 10 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 11 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 12 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 13 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 14 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 15 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 16 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

REFERENCE 17 (bases 1 to 1135)
Roest-Crollius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,

Drosophila melanogaster genome survey sequence TET3 end of BAC # Drosophila melanogaster library from Drosophila melanogaster (fruit fly) genomic survey sequence.

AL061936
AL061936.1
GI:4940214

fruit fly. *Drosophila melanogaster*
 Insecta; Hexapoda; Tracheata; Arthropoda; Metazoa; Eukaryota; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea, *Drosophilidae*, *Drosophila*.
 (bases 1 to 1101)

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pierle de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	source	Location/Qualifiers
1..1101		/organism="Drosophila melanogaster"
		/db_xref="taxon:722"
		/clone_lib="RPC1-98"
		/clone="BACR05N11"
		/notes="end : TET3"

BASE COUNT	631 a	7 c	28 g	289 t	146 others
ORIGIN					

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Best Local Similarity 40.3%; Pred. No. 0.0081;
Matches 328; Conservative 43; Mismatches 437; Indels 6; Gaps 2;

	Accession	Sequence	Length
484	tc	caaaagacatcttaaatcaaatgataatttaaggaagaagaatacagaaaaagtcag	543
78	tn	naaaanawfakaaatnataatTTTTTAATTTAAAKAKWDTAATAAAAANAAAAAAA	137
544	aa	aaatggtggaagccgcgcatcatcaagaagatgaattacatatatttcgcgttcggtt	603
138	ag	tggttttcattgaaggttttaaaaaaanaaaaaaanaaaanctnnnncnnaa	197
604	at	ggaagatcacatctgaaacaaagattttagatagagagacgatttttatcat	663
198	na	aaaaanaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa	257
664	cg	tataactataaagatcgtccgcgtaccactagcgtatattgatttaatgca	723
258	aa	aaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa	317
724	ta	ttagcagcagcgaagcgcaagcctttaaaagaataatgcataagcagat	783
318	ca	aaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa	377
784	aa	gacatgcacagcgtccctgaaatcgagaagcgcataataaaagaataattgag	843
378	aa	aaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa	437
844	ca	caactagacgcgaatcaagctcaataaaagaagcagaacattgcaacttaaac	903

/db_xref="taxon:99883"
 /clone="208P24"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG208DH12SP1-end :
 pUC-Orig"

BASE COUNT	863 a	65 c	43 g	124 t	40 others
ORIGIN					

Query Match 6.0%; Score 77.6; DB 12; Length 1135;
Best Local Similarity 43.1%; Pred. No. 0.0061;
Matches 341; Conservative 14; Mismatches 435; Indels 2; Gaps 1;

[illegible]

RESULT 2
CNS0021J
LOCUS

Page 3

BASE COUNT	516 a	67 c	22 g	120 t	160 others
ORIGIN	/clone_11b="PTB Chimpanzee Male BAC Library"				
Query Match	5.8%; Score 75.2; DB 12; Length 885;				
Best Local Similarity	36.0%; Pred. No. 0.015;				
Matches 209; Conservative	0; Mismatches 372; Indels 0; Gaps 0;				
Oy	310	tattaccgaatgtaaagcgaacacatgatgctgtaagatgattgaaagatgacgacgac	369		
Db	83	TATNNANNGNNNNCCAAANNAATATGAGNNNANNGNNANNAANNAAGNANNNNAN	142		
Oy	370	tggcttttgtaaatgctgcgaattaacttgcgaactgaaggttccacaatcggtt	429		
Db	143	ANNNAATNGNNAANNAATTTAANNAANNAANNAANNAATTTANNAANNAANNAANNA	202		
Oy	430	gatacataagcgaactcgcttcatctcgtcgcgatgattgaaataaacatcaaa	489		
Db	203	ANNAANNAANNAANGANTTTNNNANNAANNAANNAANNAANNNNANNAANNAANNA	262		
Oy	490	gacatcttaaatcaatcgataatttaagagaagaatcacgaanaagcacgaanaa	549		
Db	263	NAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA	322		
Oy	550	gggtgaagtcgcgtatcctaagcgaatgaattacatacttccgttcgtttagaa	609		
Db	323	NNNANNNANNNANNNANNAANNAANNAANNAANNTTTNTTANNNANNTTAATTA	382		
Oy	610	gatacatcgaaacaaagatttctgagatgagaatgacgattttatcatcgtatg	669		
Db	383	TNNAATTTTATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	442		
Oy	670	aatacactaagaatcgctgcgcgacacacatgatatgatttaatgcatatta	729		
Db	443	ATATTTATTTATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA	502		
Oy	730	gcagagctcaacacatgaaagcgcaagacttaaaagaagaatgcgaagcgaataag	789		
Db	503	NNANNAANNAANNTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	562		
Oy	790	atccgcaagcgtctcgaataatcagaagccataataaagaagaattctgacgaaca	849		
Db	563	AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA	622		
Oy	850	ctagaagcgaatcaagctcaataataaagaagcgcaaacatt	890		
Db	623	ANNAANGAAGCAAAATTAANNAANNAAGAAATTTATTAATTT	663		
RESULT 4					
CNS0152H	614 bp DNA linear GSS 26-JUL-1999				
LOCUS	CNS0152H				
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC				
ACCESSION	BACN12M03 of DrosBAC library from Drosophila melanogaster				
VERSION	AL104915				
KEYWORDS	fly; genomic survey sequence.				
ORGANISM	Drosophila melanogaster				
SOURCE	fruit fly				
	arthropoda: tracheata: hexapoda: insecta;				

[illegible][illegible]

us-09-509-234c-48.rst

Fri Jun 21 08:38:25 2002

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Db 404 AKGAAAAA... 894 bp DNA linear GSS 26-JUL-1999
Qy 608 asgatacatctgaaacaaagatttttagatagatgacgattttattatcatcgta 667
Db 344 CAATDA... 894 bp DNA linear GSS 26-JUL-1999
Qy 668 tgaatactataaagatcggtccgcgtaccactagctgtatattgatttgaatgcatt 727
Db 284 NAAAAA... 894 bp DNA linear GSS 26-JUL-1999
Qy 728 tagcagagctcaacactgagcgcaagactttaaaagaaattgcaaaagcagataaag 787
Db 224 AAAAAA... 894 bp DNA linear GSS 26-JUL-1999
Qy 788 acatgacagcgctccgtaagcgaagcctaaataaaagaaaatttagagcaac 847
Db 164 AAAAAA... 894 bp DNA linear GSS 26-JUL-1999
Qy 848 aactagaacgaatcaagctaaataaagcagacattgcaacttaaac 902
Db 104 AAAAAA... 894 bp DNA linear GSS 26-JUL-1999

RESULT 8
LOCUS CNS018BG 894 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
BACN13816 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL109126
VERSION AL109126.1 GI:5629430
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 894)
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (BDGP) -
http://www.edgp.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES
Location/Qualifiers
1..894
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone.lib="DrosBAC"
/clone="BACN13816"
/note="end : 77"
BASE COUNT 452 a 101 c 85 g 138 t 118 others
ORIGIN
Query Match 5.5%; Score 71.8; DB 12; Length 894;
Best Local Similarity 38.4%; Pred. No. 0.051;
Matches 170; Conservative 55; Mismatches 218; Indels 0; Gaps 0;
Qy 470 ttgaataaacaacatacaagacattttaaataatgataatttaagaaagaaata 529
Db 27 TTATWATY... 894 bp DNA linear GSS 26-JUL-1999
Qy 530 cgaataaagtcagaaagatggtgaaagtcgctatcctaaacgaagatgattacata 589

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Db 87 AAAAAA... 990 bp DNA linear GSS 03-JUN-1999
Qy 590 ttctcgttcgtttatggaagatacatctgaaacaaagatttttagatagatgacg 649
Db 147 TTGGCA... 990 bp DNA linear GSS 03-JUN-1999
Qy 650 atttttatcatcgctagaaatactataaagatcggtccgcgtaccactagctata 709
Db 207 WACRTM... 990 bp DNA linear GSS 03-JUN-1999
Qy 710 ttgattttaatgcattattagcagagctcaacactgaagcgcaagcatttaaaagaaa 769
Db 267 AAAAAA... 990 bp DNA linear GSS 03-JUN-1999
Qy 770 ttgcaaaagcagataaagacatcgacacagcgctcctgaaatcagaagccataataaa 829
Db 327 AAAAAA... 990 bp DNA linear GSS 03-JUN-1999
Qy 830 agaaaatttagcagcaacactagcgaagcgaatcaagctaaataaaagcagaaacat 889
Db 387 WAGAAA... 990 bp DNA linear GSS 03-JUN-1999
Qy 890 tgcaacttaaacacacggtgacaca 912
Db 447 AAAAAA... 990 bp DNA linear GSS 03-JUN-1999

RESULT 9
LOCUS CNS00601/c 990 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14J23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL065624
VERSION AL065624.1 GI:4944693
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 990)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
1..990
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone.lib="RPCI-98"
/clone="BACR14J23"
/note="end : TET3"
BASE COUNT 158 a 51 c 40 g 592 t 149 others
ORIGIN

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Query Match	5.5%	Score 71.8;	DB 12;	Length 990;
Best Local Similarity	37.8%;	Prod. No. 0.049;		
Matches 297;	Conservative	56;	Mismatches 452;	Indels 0;
				Gaps 0

Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidae; Anopheles.
1 (bases 1 to 879)

TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000)
Genoscope - Centre National de Sequencage
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage
dn_101_01006_FVRV Cedex - FRANCE (E-mail : segrete@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

REFERENCE
2 (bases 1 to 879)
Foth, C. W., Prev, P. T., Ke, Z., Collins, F. H. and Weissenbach, J.

TITLE Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr
JOURNAL Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr
BBMI Institut Pasteur, 25, rue du Dr
France Institut Pasteur, 25, rue du Dr
75015 Institut Pasteur, 25, rue du Dr

COMMENT
This clone is from an A. gambiae Ballybrary provided by F. H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of insects, Institut Pasteur.

FEATURES	Location/Qualifiers
source	1. .879

	note	end	:	27	
BASE COUNT	66 a	38 c	1 g	670 t	104 others
ORIGIN					

Query Match	Score	DB	Length
5.58;	71.4;	12;	879

Best Local Similarity 43.0%; Pred. NO. 0.055;
Matches 185; Conservative 37; Mismatches 207; Indels 1; Gaps. 1

473 aaataaacatcaaaagacatcttaatacaaatgataattaaaggaagaagaalacga 532

Db 645 AAAAAAAAAAGRTATATAKKAWKAWGAAAAAAAAKKGAAAAATTGWWGKTDAAAAAATTAGA 586

QY

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533 aaaggtacgaaanaatcgttgtgaagtccgcatactcaagaagatgatattaccatcatc    574  
||||| : |||| : | : ||| || : ||| ||  
||||| : |||| : | : ||| || : ||| ||
```

Db 585 AAAAAAAAAAGAGAGWKAGGKRGARAAAAGAGAKKAA-KAAAAAAAAAIGITAKKAKION 52

[illegible]

Db 526 AAAAAAAAAAKKATRRAAAAAAAMKKAGDAANAARWAGGGGAAATTCCTTA
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[illegible][illegible][illegible]

773 caaatacacaataaagacatcgcacaagcgtcctcgtaaaatacagaagaacataataaaaaga 83

[illegible]

833 aaaaatttagcacaactagaaagcgatcaagctaaataaaagaagcagaacattgc 89

[illegible]

QY 893 aacttaaca 902

Db 226 AAAAAAAAAA 217

Accession	Length	Model	EST
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U00002	11	linear	28-JAN-2002
U00003	11	linear	28-JAN-2002
U00004	11	linear	28-JAN-2002
U00005	11	linear	28-JAN-2002
U00006	11	linear	28-JAN-2002
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U00008	11	linear	28-JAN-2002
U00009	11	linear	28-JAN-2002
U00010	11	linear	28-JAN-2002
U00011	11	linear	28-JAN-2002
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U00013	11	linear	28-JAN-2002
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U00081	11	linear	28-JAN-2002
U00082	11	linear	28-JAN-2002
U00083	11	linear	

LOCUS	B2671200
DEFINITION	OP20714 Mixed stage EST's from <i>Globodera pallida</i> , the potato cyst nematode <i>Globodera pallida</i> cDNA, mRNA sequence.

ACCESSION BM415636
VERSION BM415636.1 GI:18382435

[illegible]

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Query Match          5.5%; Score 71; DB 12; Length 834;
Best Local Similarity 38.8%; Pred. No. 0.069;
Matches 167; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
473 aaataaacatcaaaagacattcttaaatcaaatgggataatttaagggaagaagaatacga 532
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT	13
LOCUS	CNS00396/c
DEFINITION	1101 bp DNA linear GSS-03-JUN-1999 Drosophila melanogaster genome survey sequence T873 end of BAC # BACR08k10 of RGC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL063921
VERSION	AL063921.1 GI:4941778
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyceta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

[illegible]

RESULT 14
 BM415686/c 966 bp mRNA linear EST 28-JAN-2002
 LOCUS
 DEFINITION OP20766 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 Globodera pallida.
 Globodera pallida.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
 1 (bases 1 to 966)
 Heer, J., Sosinski, B., Pokrzywa, R. M., Warry, A. and Opperman, C.
 Mixed Stage EST's from Globodera pallida, the potato cyst nematode
 Unpublished (2001).
 JOURNAL
 COMMENT
 Contact: Opperman, C
 Center for the Biology of Nematode Parasitism

us-09-509-234c-48.rst

Db	479	KEITKEAATAAAGAGDAMKAGDGGGAGGAGKCKKAGATATTAATTAAAGTATTAATAAAG	420
QY	713	attttaaagataatttagcagagctcaacactgaaagcgcaagactttaaaagaattg	772
Db	419	ATKKKAAAGACAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	360
QY	773	caaaagcagataaagacatcgacaagcgctctgaaatcagaagccataaataaaaga	832
Db	359	AA	3000
QY	833	aaaattgagcaacaactagagcgaaatcaagctcaaaataaaagaagcagaacattgc	892
Db	299	AA	240
QY	893	aacttaaca	902
Db	239	AAAAAAAAA	230

Search completed: June 20, 2002, 14:26:57
Job time: 17727 sec

Fri Jun 21 08:38:28 2002

us-09-509-234c-52.rge

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:13:15 ; Search time 12428.6 Seconds
(without alignments)
2261.254 Million cell updates/sec

Title: US-09-509-234c-52
Perfect score: 1343
Sequence: 1 taaatttaaatagatga.....taagaggggaatagtagaa 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBankl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
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29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1343	100.0	1343	6	A97496	A97496 Sequence 52
2	1341.4	99.9	1343	1	SH12874	V12874 Staphylococ
3	875.6	65.2	1305	6	A97484	A97484 Sequence 40
4	871	64.9	1263	1	AF099962	AF099962 Staphyloc
5	871	64.9	1263	1	SHU23711	U23711 Staphylococ
6	843.4	62.8	3446	1	SAFEWA	X17688 S.aureus fa
7	835.4	62.2	303750	1	AP003133	AP003133 Staphyloc
8	835.4	62.2	346900	1	AF003362	AF003362 Staphyloc
9	831	61.9	1257	1	AF099964	AF099964 Staphyloc
10	827.6	61.6	1254	1	AF099964	AF099964 Staphyloc
11	820.2	61.1	1350	1	SSY12875	AF144661 Staphyloc
12	820.2	61.1	1371	6	A97490	AF144661 Staphyloc
13	809.6	60.3	1263	1	A97490	AF144661 Staphyloc
14	806	60.0	1263	1	AF144661	AF099965 Staphyloc
15	805.6	60.0	1260	1	AF099965	AF145332 Staphyloc
16	805.4	60.0	1263	1	AF099965	AF269697 Staphyloc
17	805.4	60.0	1263	1	AF145332	AX145015 Sequence
18	803.2	59.8	4434	1	AF269697	AX145015 Sequence
19	803.2	59.8	4434	6	AX145015	I33344 Sequence 1
20	802.8	59.8	1257	6	I33344	U23713 Staphylococ
21	800	59.6	1877	1	SEU23713	A97488 Sequence 44
22	791.2	58.9	1295	6	A97488	A97488 Sequence 42
23	787.6	58.6	1280	6	A97486	AF145333 Staphyloc
24	774.2	57.6	1260	1	AF145333	U66880 Staphylococ
25	757.4	55.7	1263	1	SSU66880	AX141471 Sequence
26	747.8	55.7	1179	6	AX141471	A97445 Sequence 1
27	733	54.6	1328	6	A97445	AF099967 Staphyloc
28	697.4	51.9	1266	1	AF099967	AF144662 Staphyloc
29	687.8	51.2	1266	1	AF144662	A97492 Sequence 48
30	681	50.7	1297	6	A97492	AF099966 Staphyloc
31	645.4	48.1	1254	1	AF099966	A97494 Sequence 50
32	626.4	46.6	1284	6	A97494	AF269316 Staphyloc
33	467	34.8	3115	1	AF269316	AX144666 Sequence
34	467	34.8	3115	6	AX144666	AF093750 Staphyloc
35	364.8	27.2	1805	1	AF093750	AB000222 Staphyloc
36	355.6	26.5	1327	1	AB000222	U23714 Staphylococ
37	350	26.1	1551	1	SEU23714	AF106849 Staphyloc
38	349	26.0	297850	1	AP003137	AP003137 Staphyloc
39	349	26.0	341350	1	AP003365	AP003365 Staphyloc
40	349	25.9	1254	6	AX141473	AX141473 Sequence
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42	345.4	25.5	1260	1	SHU23712	U23712 Staphylococ
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44	341.2	25.4	54064	2	AC090968	AP003361 Staphyloc
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ALIGNMENTS

RESULT 1
LOCUS A97496 1343 bp DNA linear PAR 26-JAN-2000
DEFINITION Sequence 52 from Patent WO916780.
ACCESSION A97496
VERSION A97496.1 GI:6780842

KEYWORDS
SOURCE Staphylococcus hominis.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Staphylococcus.

REFERENCE
1 (bases 1 to 1343)
Bacillus/Staphylococcus group; Staphylococcus.

AUTHORS
Gala, J. and Vannuffel, P.
GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

JOURNAL
PATENT: WO 9916780-A 52 08-APR-1999;
GALA JEAN LOC (BE); UNIV LOUVAIN (BE)
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Qy	901	caaaataaaaaataaatttagaacagcaaatataaagcaaatgagcaaaaaatctatgaa	960
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Db	961	GCAACACAACCTCAATTAGAACATGATAACGAATACCAATATCTGCTGGATTTCTCTTT	1020
Qy	1021	attaatccattggaagttgatatattatgcaggtggaaagctcaaatataatatagacacttc	1080
Db	1021	ATTAATCCATTTTGAAGTTGTATATTATGCAGTGGAACTCAATTAATAATATAGACACTTC	1080
Qy	1081	gctggaagttatgcagttcaatggactatgaattatgcgaattgatcatggcattgac	1140
Db	1081	GCTGGGAAGTTATGCAGTTCAAATGGACTAATGATGATTAATATGCAAATGATATGCCATTGAC	1140
Qy	1141	ggttataattttatgggattagtgctcattttacagatgatgctgaaagatgcaggtgtt	1200
Db	1141	CGTTATATATTTTTATGGGATATAGTGGTCATTTTACAGATGATGCTGGAAGTGCAGGTGTT	1200
Qy	1201	gtaaaaattaaaaaaggatttaatgcagatgataatgaatatgttggtgatttcgtaaa	1260
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Qy	1261	cctataaataaaccaatgatttaccataatacaacacttaaaaaattaaaaagagattg	1320
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Db	1321	AATTAAGAGGGGAATAGTGAGAA	1343

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RESULT      2
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LOCUS      1343 bp DNA linear
DEFINITION      Staphylococcus hominis femA gene.
ACCESSION      Y12874
VERSION      Y12874.1 GI:2462667
KEYWORDS
SOURCE
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                  Bacteria; Firmicutes; Bacillus/Clostridium group;
                  Bacillus/Staphylococcus group; Staphylococcus.
  REFERENCE      1 (bases 1 to 1343)
                  Vannuffel,P.
                  Unpublished
  JOURNAL
  AUTHORS
  REFERENCE
  TITLE
  JOURNAL
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Query Match	99.9%	Score 1341.4	DB 1	Length 1343
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BASE COUNT 513 a 165 c 222 g 405 t
ORIGIN

Query Match 65.28; Score 875.6; DB 6; Length 1305;
Best Local Similarity 80.5%; Pred. No. 1.7e-108;
Matches 1025; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

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Db 61 TATAGTCATTTCACAAATGACTGAAACTATGAGATGAGTGAAGTTGCCAATTAACAGAA 120

QY 181 actcatttagtaggaattaaaaataagataatgaagtcattgctgttctgtatgctaact 240
Db 121 ACTCACCTTAGTTGGTATAAAAATAAAGATAATGAGTTTATTCGAGCCTGCATGTTGACA 180

QY 241 gctgtacccttatgaaatttttaaatatttttttattcaaatcgtgtccagtcattgat 300
Db 181 GCAGTACCAGTCATGAAATTTTAAAGTACTTTTATCTTAACCGAGGACCTGTAATTGAT 240

QY 301 tatgaaacaaagaaactggttcactttttttaaagaaataagtaaatatttaaaacaa 360
Db 241 TATGATAATAGAGAGCTGTTTCACCTTTCTTTTAAGTAAAGTTAAACAGTATTAAACAG 300

QY 361 caacattgtttatagctatgacaccttatttgccttatcaatatcgttaactgat 420
Db 301 CATTAATGCTATATGTTTCGAGTGCACCTTATTACCAATATCATATTTAATCATGAT 360

QY 421 ggtgattacaggaatactgtgggaatgattggtttcttcgataaaatgaacaattagaa 480
Db 361 GGTGAATATACAGTAATGCTGTAATGATTGTTCTTTGATAAGATGAAGCATCTCGGA 420

QY 481 tatacaacaaaggggtttacaacagattgacccaataattcaaatcgtgtccattca 540
Db 421 TTGCAACATGAAGGCTTTACTAAGGTTTGTATCCGATTAAACAAATCCGATATCATCT 480

QY 541 gttttaatttaagataaaaactcctaaagatgatttaaatggaatgagtagttacga 600
Db 481 GTTTAGATTAAAAAATAAACATCTAAAGATATATTAAATGGAATGATAGTACGT 540

QY 601 aaaaagaatactaaaaaagctccaaaataatggtttaagtaagattttcttactaaga 660
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QY 661 gaattacatttttcogatacatttatgaagatacatcagagactaaagaattttctgat 720
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QY 721 agagagagatttttttactaatcgtattgattcatttttaagataagattagtagtacct 780
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QY 841 aataagacttaacaaagctcctaaagattttgaaaaacgacagataacaaaaagca 900
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Db 1261 AATTAAGAGGGGA 1274

RESULT 4
AF099962 1263 bp DNA linear BCT 02-NOV-1998
LOCUS Staphylococcus haemolyticus factor essential for methicillin
DEFINITION resistance FEMA (fema) gene, complete cds.
ACCESSION AF099962
VERSION AF099962.1 GI:3820623
KEYWORDS Staphylococcus haemolyticus.
SOURCE Staphylococcus haemolyticus.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1263)
AUTHORS Vannuffel,P., Heusterspreute,M., Bouyer,M., Philippe,M. and Gala J.-L.
TITLE Molecular characterization of femA from Staphylococcus hominis, Staphylococcus saprophyticus and Staphylococcus haemolyticus and femA-based discrimination of staphylococcal species
JOURNAL Res. Microbiol. (1998) In press
REFERENCE 2 (bases 1 to 1263)
AUTHORS Vannuffel,P., Heusterspreute,M. and Gala,J.-L.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1998) LBCM, UCL, Cios Chapelle-aux Champs 30/3046, Bruxelles 1200, Belgium
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Page 5

Query Match	64.98;	Score 871;	DB 1;	Length 1263;
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Matches 1018;	Conservative	0;	Mismatches 245;	Indels 0;
			Gaps	0;

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Db	61	AGCATTTTACCAAAATGACTGAAACCTTGAGATGAAAGTGTGCAATATTAACCGAAACT	120
Oy	184	catttgtagaattaaataaataagaatagaagcattgcgtgattgtactaagtc	243
Db	121	CACCTAGTTGGTAATAAAATAAAGAAATAGAGTTATGACGCTGCAATGTTGACAGCA	180
Oy	244	gtaccggcttaagaaattttaaattttttttaaactgtgtggtccagtcattgattat	303
Db	181	GTACCGAGCATAAATTTTAAATGCTTTTATCTTAAACGAGGACCTGTAATTAATTAAT	240
Oy	304	gaataaagaagactgcgttcacttttctcttaacgataaaglaataattttaaacaaca	363
Db	241	GATATAAGAGACTGTTGCACTTTTCTTTTAATGAGTTAAACAAGATTTTAAACAGCAT	300
Oy	364	cattgtttatgtacgtatagacccttattgtccctatcgaatcgtlaactaagtc	423
Db	301	AATGCTATATGTTGCGATGGAGCTTACCTATTACATATCAATTTTAAATCTAGTGGT	360
Oy	424	gattacaggaatagcggggagatgtgttcttcgttaaatgaagaacattagat	483
Db	361	GAAATTCACAGTAAGCTGGTAATGATTTGTTTGATTAAGATGAAGCATCTCGGATTT	420
Oy	484	caacagaaggggttcaacaggaatttgaccataataccaattcggctcattcagtc	543
Db	421	GAAATTAAGCTTACATAAGGTTTGTATGCGATTAACAAATCCGATATCACTTGCTGT	480
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Oy	604	agaatcctaaagaagtccaaaaaatggtgtcaagtagaatttcttaataagaagaa	663
Db	541	CGTAATATCTAATAAAGTTCAAAAAATGCTGTGAAGTTAAGTTTATCGAAGAAGAA	600
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Db	601	CTTCCAACTTCGCTTCATTTATGGAATATCAACGAAACGAAAGATTTCAAGATAGA	660
Oy	724	gaggatagtttctacataatcgatttgatcatatttaagaatagatgaattgaactcttc	783
Db	661	GATGTAATCTTCTATTAATAATGCTATGCAATTTCAAAAGTACAGTCTGTATACCACTA	720
Oy	784	gatatataaaatttgatgatactcttgaagaacttcattatgcagaaagtcagacattaat	843
Db	721	GCTTTATTAAGTTTGATGATGATCAATCGAAGAAATTACAAATTAACGTAACCTTTAAAT	780
Oy	844	aaagacttaacaaagctcctaagaatattgaanaagcccgataaanaaagaagcaca	903
Db	781	AAAGATGTTAATAAGCTTTAAAGATTAATGAAAAAGCAACACATATAAAGGCAATTT	840
Oy	904	aataaaaaataaatttagaagcgcataataaagaacaatgagaanaaatttgatgaaga	963
Db	841	AATTAATAAAGAAATCTTGAAAAACATTAATGATGCCAATCAACAAAAATTAAGAGAGCT	900
Oy	964	acccaacttcaattagacatgylaaagaaathacaatatcgtcgtgattcttcttatt	1023

[illegible]

BASE COUNT 492 a 162 c 214 g 395 t
ORIGIN

Query Match 64.9%; Score 871; DB 1; Length 1263;
Best Local Similarity 80.6%; Pred. No. 7e-108;
Matches 1018; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

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QY 124 agccattttacacagatgactgaaattatgagtttaaaagtgtcgagaacactgaact 183
DB 61 AGTCATTTCACACAAATGACTGAAACTATAGATGAAGAGGTGCAATAAAGACAGAACT 120
QY 184 catttagtaggaattaaaaataaagataaagtcattgctgttctgctgaactgct 243
DB 121 CACTTAGTTGGTATATAAATAAAGATTAAGTATGAGTTTATGAGCTGCATGTTGACAGCA 180
QY 244 gtaccggttatgaaaatttttaaatatttttttcaaatcgtgtccagtcattgattat 303
DB 181 GTACCACTCATGAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTT 240
QY 304 gaaacaaagaactogtctcaacttttttttcaacgaatttaagtaaatatttaaacacaa 363
DB 241 GATAATAGAGAGCTTGTTCACCTTTTCTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTT 300
QY 364 cattgtttatatgaagtacagaccatttttgccttatcaaatatcgtatcatcgtatgct 423
DB 301 AATTGTCTATATGTTGAGTGTGACCTTTATTTACCATATCAATATTAATATCATGATGCT 360
QY 424 gatattacaggaatctgggaatgattgtcttcgataaaatgaacaaataggatgat 483
DB 361 GAATTTACAGTANTGCTGTTGATGATGTTGTTTGTATGATGATGATGATGATGATGATGAT 420
QY 484 caacacgaagggtttcaacagagatttgatccaatattcaaatcgtgtccagtcattcagtt 543
DB 421 GAACATGAAGCTTTTACTAAAGTTTGTATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 544 ttaatttaagagataaaactgctaaagatgatttaaatggaatggaatgatttactaga 603
DB 481 TTAGATTAAAAATAAATCACTAAAGATATATAAATGGAATGGAATGGAATGGAATGGAATGGAAT 540
QY 604 gaaataactaaaagctccaaaaatggtgttaaaagtaagattttcttactaaagaagaa 663
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ACCESSION X17688.1 GI:46579
VERSION X17688.1
KEYWORDS femA protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 3446)
AUTHORS Berger-Baechli, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3446)
AUTHORS Berger-Baechli, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
TITLE femA, a host-mediated factor essential for methicillin resistance in Staphylococcus aureus: molecular cloning and characterization
JOURNAL Mol. Gen. Genet. 219 (1-2), 263-269 (1989)
MEDLINE 90136516
COMMENT Draft entry and computer-readable sequence for [1] kindly provided by B. Berger-Baechli, 11-APR-1989.
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LOCUS Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
DEFINITION Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
ACCESSION AP003133 BA000018
VERSION AP003133.2 GI:14349175
KEYWORDS
SOURCE
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ORGANISM Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
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Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,T.,
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Fri Jun 21 08:38:28 2002

Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*
Lancet 357 (9264), 1225-1240 (2001)
21311952
2 (bases 1 to 303750)
Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
Direct Submission
Submitted (30-JAN-2001) Kenichi Aoki, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara Shibuya-ku, Tokyo 151-0066, Japan
(E-mail:aoki-kenichi@meti.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1972, Fax:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701012.

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DEFINITION	Ap003362 Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete sequence, section 5/9.	DNA linear ECT 07-FEB-2002
ACCESSION	AP003362 BA000017	
VERSION	AP003362.2 GI:14247083	
KEYWORDS	. Staphylococcus aureus subsp. aureus Mu50 (sub-species:aureus Mu50, strain:MU50) DNA. . Staphylococcus aureus subsp. aureus Mu50 Bacteria; Firmicutes; Bacillus/Clostridium group;	
SOURCE		
ORGANISM		

Bacillus/Staphylococcus group: Staphylococcus.

1 (sites)
Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Uji,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of methicillin-resistant Staphylococcus
aureus
Lancet 357 (9264), 1225-1240. (2001)
21311952
2 (bases 1 to 346900)
Ohta,T. Submission
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology; 1-1-1 Ten-nodai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohtasakura.cc.tsukuba.ac.jp. Tel:81-298-53-3454,
Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13875626.
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ORGANISM Staphylococcus capitis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/staphylococcus group; Staphylococcus.

REFERENCE 1 (bases 1 to 1254)
AUTHORS Vanuifel, P., Heusterspreute, M., Bouyer, M., Philippe, M. and Gala, J.-L.

TITLE Molecular characterization of fema from Staphylococcus hominis, Staphylococcus saprophyticus and Staphylococcus haemolyticus and fema-based discrimination of staphylococcal species

JOURNALS Res. Microbiol. (1998) In press

REFERENCE 2 (bases 1 to 1254)
AUTHORS Vanuifel, P., Heusterspreute, M. and Gala, J.-L.

TITLE Direct Submision
JOURNALS Submitted (21-Oct-1998) LBCM, UCL, Clos Chapelle-aux Champs 30/3046, Bruxelles 1200, Belgium

FEATURES
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ORIGIN

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ACCESSION Y12875
VERSION Y12875.1 GI:2462696
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SOURCE Staphylococcus saprophyticus.
ORGANISM Staphylococcus saprophyticus
REFERENCE 1 (bases 1 to 1350)
Bacillus/staphylococcus group; Staphylococcus.

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		Bacillus/Staphylococcus group; Staphylococcus.		

REFERENCE 1 (bases 1 to 1371)
 AUTHORS Gala, J. and Vannuffel, P.
 TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
 DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 JOURNAL Patent: NO 9916780-A 53 08-APR-1999;
 GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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 Matches 1008; Conservative 0; Mismatches 313; Indels 0; Gaps 0:

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RESULT 13

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 DEFINITION Sequence 46 from Patent WO9916780.
 A97490
 VERSION A97490.1 GI:6780836
 KEYWORDS

SOURCE

Staphylococcus capitis.
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.

REFERENCE

1 (bases 1 to 1283)
 AUTHORS Gala, J. and Vannuffel, P.
 TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
 DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 JOURNAL Patent: NO 9916780-A 46 08-APR-1999;
 GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
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LOCUS
DEFINITION Staphylococcus aureus subsp. anaerobius factor essential for
methicillin resistance (fema) gene, complete cds.
ACCESSION AF144661
VERSION AF144661.1 GI:4929298
KEYWORDS
SOURCE Staphylococcus aureus subsp. anaerobius.
ORGANISM Staphylococcus aureus subsp. anaerobius
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
AUTHORS 1 (bases 1 to 1263)
TITLE Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
Cloning and characterization of femA genes from Staphylococci
JOURNAL species
REFERENCE 2 (bases 1 to 1263)
AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE Direct Submission
JOURNAL Submitted (21-APR-1999) LBCM, UCL 3046, Clos Chapelle-aux-Champs,
30, Bruxelles 1200, Belgium
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Best Local Similarity 77.4%; Pred. No. 3.5e-99;
Matches 977; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

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DEFINITION      Staphylococcus lugdunensis factor essential for methicillin
ACCESSION      AF099963
VERSION      AF099963.1 GI:3820625
KEYWORDS
SOURCE      Staphylococcus lugdunensis.
ORGANISM      Staphylococcus lugdunensis
REFERENCE
AUTHORS      Vannuffel, P., Heusterspreute, M., Bouyer, M., Philippe, M. and Gala
J. -L.
TITLE      Molecular characterization of femA from Staphylococcus hominis,
JOURNAL      Staphylococcus saprophyticus and Staphylococcus haemolyticus and
REFERENCE      femA-based discrimination of staphylococcal species
AUTHORS      Res. Microbiol. (1998) in press
TITLE      2 (bases 1 to 1260)
JOURNAL      Vannuffel, P., Heusterspreute, M. and Gala, J. -L.
AUTHORS      Submitted (21-OCT-1998) IBCU, UCL, Clos Chapelle-aux Champs
JOURNAL      30/3046, Bruxelles 1200, Belgium

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Fri Jun 21 08:38:28 2002

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GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:46:55 : Search time 1139.49 seconds
(without alignments)
2023.551 Million cell updates/sec

Title: US-09-509-234c-52

Perfect score: 1343
Sequence: 1 taaattttaaataatgca.....taagaggggaatagtaga 1343

Scoring table: IDENTITY_MTC
Gapop 10.0 : Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /N_Geneseq_032802:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1331	99.1	1342	20	AA37804
2	875.6	65.2	1305	20	AA37798
3	820.2	61.1	1371	20	AA37805
4	809.6	60.3	1283	20	AA37801
5	803.2	59.8	1257	22	AA54373
6	802.8	59.8	1257	15	AA078141
7	791.2	58.9	1295	20	AA37800
8	787.6	58.6	1280	20	AA37799
9	747.8	55.7	1179	22	AA52400

10	733	54.6	1328	20	AA37797	Staphylococcus sp.
11	681	50.7	1297	20	AA37802	Staphylococcus sch
12	626.4	46.6	1284	20	AA37803	Staphylococcus set
13	467	34.8	3115	22	AA53994	S. epidermidis gen
14	368.8	27.5	3271	18	AA74747	Staphylococcus aur
15	348.4	25.9	1251	15	AA074775	Staphylococcus epi
16	347.6	25.9	1254	22	AA52401	S. epidermidis ope
17	345.4	25.7	6528	21	AA49723	Staphylococcus sim
18	337.6	25.1	1245	23	AA55125	Staphylococcus aur
19	336	25.0	1470	20	AA22843	Staphylococcus aur
20	336	25.0	1470	20	AA219882	Staphylococcus aur
21	330.4	24.6	1260	20	AA37808	Staphylococcus aur
22	330.4	24.6	1260	20	AA37801	Staphylococcus aur
23	327.2	24.4	1260	23	AA54419	Staphylococcus aur
24	325.8	24.3	1257	23	AA51636	Staphylococcus aur
25	323.6	24.1	3821	18	AAV74615	S. epidermidis gen
26	313.6	23.4	2453	22	AA55015	Essential Staphylo
27	278.8	20.8	453	21	AA426858	Staphylococcus aur
28	278.8	20.8	453	22	AA508009	Staphylococcus aur
29	278.8	20.8	453	22	AA591540	Staphylococcus aur
30	251.2	18.7	410	21	AA326855	Essential Staphylo
31	251.2	18.7	410	22	AA308006	Staphylococcus aur
32	251.2	18.7	410	22	AA591537	Staphylococcus aur
33	243.6	18.1	420	20	AA387951	Synthetic DNA frag
34	241.6	18.0	514	18	AA50799	Staphylococcus aur
35	232.4	17.3	400	21	AA326853	Essential Staphylo
36	232.4	17.3	400	22	AA508004	Staphylococcus aur
37	232.4	17.3	400	22	AA591535	Staphylococcus aur
38	197.4	11.7	1221	18	AAV74940	Staphylococcus aur
39	186.6	11.9	795	23	AA550908	Enterococcus faeca
40	160.8	12.0	1281	23	AA552835	C. glutamicum SRT
41	153.6	11.4	543	22	AA571123	Enterococcus faeca
42	142.8	10.6	10194	20	AA313028	Staphylococcus aur
43	136.2	10.1	6804	20	AA376160	Staphylococcus aur
44	129.2	9.6	1230	20	AA576141	zif protein with z
45	128.4	9.6	3000	22	AA20311	Streptococcus pneu

ALIGNMENTS

RESULT 1

ID AA37804 standard; DNA; 1342 BP.

XX AA37804:

XX 09-JUL-1999 (first entry)

XX Staphylococcus hominis FemA DNA.

XX FemA: identification; detection; therapy; infection; femB:

KW amplification; genotyping; gram-positive bacteria; vaccine; ss.

XX Staphylococcus hominis.

XX Key location/Qualifiers

XX CDS 64..1327

XX FT /*tag- a

XX FT /product- "FemA"

XX MO9916780-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-BE00141.

XX 26-SEP-1997; 97EP-0870146.

XX (BENA-) BELGIAN MIN NAT DEFENCE.

XX (UTLO-) UNIV CATHOLIQUE LOUVAIN.

XX Gala J, Vannuffel P;

Qy	1	taaaattttaaaatagtcaactcaaatataaataaaagattctaaattagggttatagag	80
Dd	1		60
Qy	61	ataatgaagtttacaaatttaacagctacagaaatttgcgattttactgaaaaatgcc	120
Dd	61		120
Qy	121	tatagccattttcacagatcgactgaaattatgagtttaaagtttgtcggaaaaactgaa	180
Dd	121		179
Qy	181	actcatatttagtaggaataaaaaataagaataaagaagtcattgctgtgatgtctaact	240
Dd	180	actcatatttagtaggaataaaaaataagaataaagaagtcattgctgtgttgatgtctaact	239
Qy	241	gctgtaccggttatgaaaaattttaaatatttttattccaatctggtgtccagtcattgat	300
Dd	240	gctgtaccggttatgaaaaatttttaaatatttttattccaatctggtgtccagtcattgat	299
Qy	301	tatgaaaaacaagaacctgcctactttttctttaagaattaagtaaatatttataaacaa	360
Dd	300	latgaaaaacaagaacctgcctactttttctttaagaattaagtaaatatttataaacaa	359
Qy	361	caacattgtttatatgtacgtatagaccttatttgccttatcatatcgttaattcatgat	420
Dd	360	caacattgtttatatgtacgtatagaccttatttgccttatcatatcgttaattcatgat	419
Qy	421	ggtgatattcacaggaaatctcgggaatgatcggcttcgtcataaaatgaacaattcaga	480
Dd	420	ggtgatattcacaggaaaTgcTgggaatgatcggcttcgtcataaaatgaacaattcaga	479
Qy	481	tatcaacacgaagggtttacacacaggtattgatccaatatatacaaaatcgggttcattca	540
Dd	480	tatcaacacgaagggtttacacacaggtattgatccaatatatacaaaatcgggttcattca	539
Qy	541	gtttttaaatttaaggaataaaactgcTtaaagatgattataatggaaatggatagtttacga	600
Dd	540	gtttttaaatttaaggaataaaactgcTtaaagatgattataatggaaatggatagtttacga	599
Qy	601	aaaagaataactaaaaaagtcocaaaaaatcgtgttaaagttaagattttctactaaagaa	660
Dd	600	aaaacraataactaaaaaagtcocaaaaaatcgtgttaaagttaagattttctctcaaagaa	659

AX	AAX37798;
AC	09-JUL-1999 (first entry)
DDT	Staphylococcus haemolyticus FemA DNA.
DE	FemA; identification; detection; therapy; infection; femB;
KW	amplification; genotyping; gram-positive bacteria; vaccine; ss.
KW	
OS	Staphylococcus haemolyticus.
OS	
XX	Key
XX	Location/Qualifiers
FH	4..1305
FT	/+tag= a
FT	/product= "FemA"
FT	
XX	
PN	W09916780-A2.
XX	
PD	08-APR-1999.

XX 28-SEP-1998; 98MO-BE00141.
 PR PF
 XX 26-SEP-1997; 97EP-0870146.
 PR
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (OYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB; AAY08215.
 PT
 PS New Staphylococcus-specific oligonucleotides
 Claim 15; Fig 6a-d; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the fema sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of fema
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 CC
 CC Sequence 1305 BP; 513 A; 165 C; 222 G; 405 T; 0 other;
 SO

Query Match 65.2%; Score 875.6; DB 20; Length 1305;
 Best Local Similarity 80.5%; Pred. No. 2e-138;
 Matches 1025; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 61 ataatgaattacaataattacagctacagaattggcgattttctctgaaataatgcca 120
 Db 1 ataatgaattacaataattacagctacagaattggcgattttctctgaaataatgcca 60
 QY 121 tatagccatttaacacagatgactgaaattatggttaaaagtctggaacactgaa 180
 Db 61 tatagccatttaacacagatgactgaaattatggttaaaagtctggaacactgaa 120
 QY 181 accatttagtaggaataaataaagaataatgaagtcattgctgctgtatgtaact 240
 Db 121 accatttagtaggaataaataaagaataatgaagtcattgctgctgtatgtaact 180
 QY 241 gctgtaccgttaagaaattttaatatattttatcaaatcgtgctcagcattgat 300
 Db 181 gctgtaccgttaagaaattttaatatattttatcaaatcgtgctcagcattgat 240
 QY 301 tatgaataacaaagaactcgttaccctttttttaagcaataatgaataatgaataa 360
 Db 241 tatgaataacaaagaactcgttaccctttttttaagcaataatgaataatgaataa 300
 QY 361 caaatgtttatagtagtaagacacatttgccttaacatcgtatcgtatgat 420
 Db 301 caaatgtttatagtagtaagacacatttgccttaacatcgtatcgtatgat 360
 QY 421 ggtgatatcaggaatgctggaatgattgttcttcgataaataatgaacattgagg 480
 Db 361 ggtgatatcaggaatgctggaatgattgttcttcgataaataatgaacattgagg 420
 QY 481 tatcaaacagaggtttacaacagatttgatccaattcaaatcgttccattca 540
 Db 421 ttgacatgagaggtttacaacagatttgatccaattcaaatcgttccattca 480
 QY 541 gtttaattaaaggaataaacgtcaaatgataatgaatgaatgattgattcga 600
 Db 481 gtttaattaaaggaataaacgtcaaatgataatgaatgaatgattgattcga 540

Db 481 gtttaattaaaggaataaacgtcaaatgataatgaatgaatgattgattcga 540
 QY 601 aaaaagaaactaaataaagtcacaaataatggtgttaagtaattcttctacagaag 660
 Db 541 aaaaagaaactaaataaagtcacaaataatggtgttaagtaattcttctacagaag 600
 QY 661 gaattccatttccagatcattatggaagatcatcatcagacagacataaatttctgat 720
 Db 601 gaattccatttccagatcattatggaagatcatcatcagacagacataaatttctgat 660
 QY 721 agagagagatttttactaataatcagatttgatcatttaagaatagatgattgatt 780
 Db 661 agagagagatttttactaataatcagatttgatcatttaagaatagatgattgatt 720
 QY 781 ctgcataataaatttgatgataatcctggaagacttcgtgagacgtcagacatta 840
 Db 721 ctgcattataatgatttgatgataatcctggaagacttcgtgagacgtcagacatta 780
 QY 841 aataagacttaacaaagctcaagatattgaaacagacacagataacaaagaagca 900
 Db 781 aataagacttaacaaagctcaagatattgaaacagacacagataacaaagaagca 840
 QY 901 caataaataaataatattagaaacagacataaagaacatgacagacaaatattgtaa 960
 Db 841 ttataataaataaataatattagaaacagacataaagaacatgacagacaaatattgtaa 900
 QY 961 gcaacacacttaacatgaaatgaaacagacataacattcctgctgattctctt 1020
 Db 901 gctaaataatcaacagacacatgaaatgaaacagacataacattcctgctgattctctt 960
 QY 1021 attaatccattgaatttatattatgacagatgacagacacataatagacacattc 1080
 Db 961 attaatccattgaatttatattatgacagatgacagacacataatagacacattc 1020
 QY 1081 gctgaagattacgaattcaatgacatgataatgaatgaatgaatgaatgaatga 1140
 Db 1021 gctgaagattacgaattcaatgacatgataatgaatgaatgaatgaatgaatga 1080
 QY 1141 cgttaataattttatggaattggtcattttcagagatgacgacgagacagaggtgt 1200
 Db 1081 agatacaatttcattgattatgacgacatgatttgaatgaatgaatgaatgaatga 1140
 QY 1201 gtaaatattaaagagatttaacgaatgaaatgaatgaatgaatgaatgaatga 1260
 Db 1141 attaaatttaaaagagatttaacgaatgaaatgaatgaatgaatgaatgaatga 1200
 QY 1261 cctataataaacaatgataatcactataacacacttaaaataaataaagaattg 1320
 Db 1201 cctataataaacaatgataatcactataacacacttaaaataaataaagaattg 1260
 QY 1321 aattaagagggaa 1334
 Db 1261 aattaagagggaa 1274

RESULT: 3
 AAX37805
 ID AAX37805 standard; DNA; 1371 BP.
 AC
 XX AAX37805;
 DE 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus saprophyticus Fema DNA.
 XX
 KW FemA; identification; detection; therapy; infection; fema;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus saprophyticus.
 XX
 FT Key Location/Qualifiers
 FT CDS 64..1326
 FT /tag= a

Fri Jun 21 08:38:29 2002

/product= "Fema"

W09916780-A2.

08-APR-1999.

28-SEP-1998; 98WO-BE00141.

26-SEP-1997; 97EP-0870146.

(BENA-) BELGIAN MIN NAT DEFENCE.

(UYILO-) UNIV CATHOLIQUE LOUVAIN.

Gala J, Vannuffel P;

WPI: 1999-287521/24.

P-PSDB; RAY08222.

New Staphylococcus-specific oligonucleotides

Claim 29; Fig 13; 48pp; English.

This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus femA nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various femA sequences which are specific to known or unknown Staphylococci species. Since the femA sequence is similar to the femB sequence, the oligonucleotides can also be used for the molecular genotyping of femB genes of different Staphylococci species or other gram-positive bacteria. The femA nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the femA nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections.

Sequence 1371 BP; 545 A; 155 C; 248 G; 423 T; 0 other;

Query Match 61.1%; Score 820.2; DB 20; Length 1371;
Best Local Similarity 76.3%; Pred. NO. 4e-129;
Matches 1008; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

QY 6 tttaaattagtcacactcaataataaagattcttaattagaggtattatagagataat 65
DB 6 tttagattagaattaaactcgaaatagaaactatagataaaatgggggtatataaaaaaat 65
QY 66 gaagtttcaaaatttaacagctacagaatttgcgattttactgaaaaaatgccatatag 125
DB 66 gaatttcaaaatttaacagctacagaatttgcgattttactgaaaaaatgccatatag 125
QY 126 ccatattcacagatgactgaaaaattatgatttaaaagtttctgtagaaactgaactca 185
DB 126 tcaatttagcgaatttcaactgcaaaaggttcggtcatttgcgataaaatgccgaatag 185
QY 186 tttagtgaatttaaaataaagaattgaattgaattgaattgaattgaattgaattgaatt 245
DB 186 cctagtaggttataagaataatgaattgaattgaattgaattgaattgaattgaattgaatt 245
QY 246 accggttatgaatttttaatt 305
DB 246 tccgttatgaatt 305
QY 306 aaacaaagaactcgttttcatt 365
DB 306 aaataaagaactcgttttcatt 365
QY 366 ttgtttatagctatagacccatttgccttatcatcatcatcatcatcatcatcatcatcat 425
DB 366 tgccttatattacaggtgtagacccatttgccttatcatcatcatcatcatcatcatcatcat 425
QY 426 tattacagaaatgctgggaatgattggtttcttcgataaaatgaacaaattaggtatcatca 485

DB 426 agtattagcaaatgcgggtcagcagattggatttttgataaaatgaacacactcgtgtataa 485
QY 486 acacgaagggtttacacacagagatttgatcccaattattacaaatcgggttccattcgtttt 545
DB 486 gcatgaagggtttttaaactggtttgacccaatacttcaataaagattccattcgtttt 545
QY 546 aaatttaagagataaaaactgctaaagatgtattaaatggaatgtagttttacgaaag 605
DB 546 agatttagctggaataaactgctaaagacgtacttaattggaatgtagttttacgaaag 605
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DB 606 aaatactaaaaagtcacaaaaaattggtttaaagtaagattttttaggtgaagatgagt 665
QY 666 acctatttcagatcattttatggaagatacatcagagactaaagaattttctgatagaga 725
DB 666 gccaatttcgcctcatttcagagatacttctgaaacaaagattttgacgatagaga 725
QY 726 ggaatgtttttactataatcgatttgatttttaagacatagatttagtacctctgcg 785
DB 726 tgacgattttttattataataggttaagataattataaagatcgtgctgtccattagc 785
QY 786 atataataaatttaataatcttgaagaacttctcagacacgtcagacattataataa 845
DB 786 ttatatggtatttgatgataataacagaattaaagcgtgaacggaagtattaaagtaa 845
QY 846 agacttaacaaagctctcaaaatgatttgaacaaacgacacagataacaaaaaacacaaa 905
DB 846 agataataaataagcagttgaagatatagaataaagacacagataaataaaacgctata 905
QY 906 taaaaataaatttagacagcgaattaaagaacaaatgacgaataaattgtgaagcaac 965
DB 906 taaaaagaataatttagacacacactgttgcaacacacacacacacacacacacacacac 965
QY 966 acaacttcaatttagacacacgttgtaacgaattaccacattctcgtggtattcttttataa 1025
DB 966 tgcgttacaagaagacgttgtaacgaattaccacgttctcgtggtattcttttataa 1025
QY 1026 tccatttgaagttgtattattatgcaggtggaacgtcaataataatagacactcgtg 1085
DB 1026 tccatttgaagttgtattattatgcaggtggaacgtcaataataatagacactcgtg 1085
QY 1086 agttatgcagtttcaattgactatgatttaattgcaattgcatggtcattgacogtta 1145
DB 1086 tagttatgcatacaatggaagatgatttaattgctatagatcatatagatagata 1145
QY 1146 taatttttgggttagtgggtcattttacagatgtagctgaagatgcaggtgtgtataa 1205
DB 1146 taatttttgggttagtgggtcatttttactgaagatgcaggaagatgcaggtgtgtataa 1205
QY 1206 atttaaaaaaggatttaacgagatgtaattgaataattggtgatttgcgttaaacctat 1265
DB 1206 atttaaaaaaggatttttaactgagatgtagtagaatagttgggtattttattaaacgat 1265
QY 1266 aaataaaccatgtatttctactatatacacacacttataaaaaatttaaaagagatgtaata 1325
DB 1266 taataagccaatgacaaaattttacacacatttatacgaattgaaaaaattaaagataata 1325
QY 1326 a 1326
DB 1326 a 1326

RESULT 4
AA37801
ID AAX37801 standard; DNA; 1283 BP.
XX AAX37801;
AC AAX37801;
XX 09-JUL-1999 (first entry)
XX Staphylococcus capitis FemA DNA.
DE

XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3737.
 DE Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW vaccination; endocarditis; ds.
 KW Staphylococcus epidermidis.
 OS WO200134809-A2.
 PN 17-MAY-2001.
 XX 09-NOV-2000; 2000WO-US30782.
 XX 09-NOV-1999; 99US-0164258.
 PR (GLAX) GLAXO GROUP LTD.
 XX Kimmerly WJ;
 XX WPI; 2001-316495/33.
 DR Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 XX useful for vaccinating against infections, e.g. endocarditis -
 PT Claim 8; Page 1358-1360; 2188pp; English.
 PS AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX Sequence 4434 BP; 1676 A; 554 C; 819 G; 1385 T; 0 other;
 SQ

Query Match 59.8%; Score 803.2; DB 22; Length 4434;
 Best Local Similarity 77.0%; Pred. No. 3e-126;
 Matches 992; Conservative 0; Mismatches 293; Indels 3; Gaps 1;
 QY 26 aattataaagaattcttaattaggaggtatagatataaagttacaaattacacag 85
 DB 2832 aaatagataaagaataaaatggaggtat---gaagatgaatttcacgaattgacag 2888
 QY 86 ctacagaatttgcgattttactgaaataatgcatatagccattttacacagatgactg 145
 DB 2889 cttaagaatttgcgattttactgacatgacatagcattttacacaaatggaag 2948
 QY 146 aaaattatgagtttaaaagtctgagaaactgaactcatttagtagggaattaaataa 205
 DB 2949 gtaattacgaattaaagtctgagaaactgaactcatttagtagggaattaaataa 3008
 QY 206 aagataatgaatttgcgattttactgacatgacatgacatgacatgacatgacatgac 265
 DB 3009 atgataacgaagtgcgatttgcgattttactgacatgacatgacatgacatgacatgac 3068
 QY 266 aatattttttacaaatgctgctcagtcattgattatgaaacaaacgaactgcttact 325

DB 3069 aatattttttatcccaatgcggtccagtaataatgattataataataaagagctgtacatt 3128
 QY 326 tttcttttaacgaataaagtaataatttttaaaacacacacacattgttttataatgacgtatag 385
 DB 3129 tttcttttaagtaattgagtaataattgtaaaaaataataattgttttataatgaggtg 3188
 QY 386 accctatttgccttatcaatgcgttaattcatcatggtgatatattacaggaataatgcggga 445
 DB 3189 accataccttcataataataatttaataatcatgagggagaaataactggaatgcagggtc 3248
 QY 446 atgattggttcttcgataaaaaatgaacaaataggatatcaacacgaagggtttcacacag 505
 DB 3249 atgattgagattttgagtaattgagaggtttaggatataaacacgaaggattccacaag 3308
 QY 506 gatttgatccaatattacaaattcgggtccattcagtttttaatttaattaaagataaaactg 565
 DB 3309 gatttgatcctgtattacaaatccgattatcatttcttcttaatttagcaacaaagtg 3368
 QY 566 cttaaagatgtattaaatggaatgagtagttttacgaaaaagaaataactaaaaaagtcacaa 625
 DB 3369 ctaatgatgttttaaaaaacatggatgggttttaagaaagcgtataatactaaaaaagttaaga 3428
 QY 626 aaaatggtgttaagtaagatttcttactaaagaagaattaccatttttcagatcattta 685
 DB 3429 aaaatggagttaagtcgcctttttatctcgaagaagattaccattatttaggtcattta 3488
 QY 686 tgaagatcacatcagacgacgataaagaattttctgatagagagatagtttttactataatc 745
 DB 3489 tggaggatacctctgaactaaagattttgcagtagagagaagatagttttttattacaaca 3548
 QY 746 gatttgatcatttttaagaatagattagtagtaccctctcgcataataaaaatttgatgaat 805
 DB 3549 gattcaaacatttaaaagccgtgttttagtaccactagcctataattactttgatgagt 3608
 QY 806 atcttgaagaacttcctcagacgctcagacattaaataaagacttaaacaaaagcctctaa 865
 DB 3609 atatagaggcaactaaataatgaagaatgtcttaataaagattataataaaagccttaa 3668
 QY 866 agatattgaaaaacgacagataacaaaaagcacaataaataaaaaataaatttagaac 925
 DB 3669 aagacattgaaacgtccagagaataaaaaagcacatacaaaaaaggaataattagaac 3728
 QY 926 agcaattaaaagcaattgagcgaacaaatgtatgaagcaacacaaacttcaattagaacatg 985
 DB 3729 acaactcgatgcgaatccagcaaaaaatttaataagctaaataaaacacgaagaacatg 3788
 QY 986 gtaacgaattacaaataatctcgtggtattcttcttttataatccatttgaagtgtatatt 1045
 DB 3789 gcaatgaattacccatctcgtggtcttcttataataatccggttgcgagtgattact 3848
 QY 1046 atcgagggtggaacgcaaaaataatagacacttcgctggaagtattatgcagttcaatgga 1105
 DB 3849 agcgtggggaacttcaaaatcgattatccatttgcagggagctatcggttcaatgga 3908
 QY 1106 ctatgatttaattatgcaattgcatggaattggaattggaatttatttgggattagtg 1165
 DB 3909 agatgattaaactgcaattgaaacatggtattaaatcggtataataattctatggtattagtg 3968
 QY 1166 gtcattttacagatgagtcggaagatgcaggtgtgttgaataatttaaaaaagcatttaag 1225
 DB 3969 gtgacttttagtgaagatgcgtgaagatgcgtggtggttaggttcaaaaagggtctatgatg 4028
 QY 1226 cagatgtaattgaataatgttgggtgatttctgttaaaccttataataaaccaatgtattcac 1285
 DB 4029 ccgagtgttatagaataatggttgggtgaactttattaaactattataaaccaatgtataaca 4088
 QY 1286 tatatacaacacttaaaaaataaaaaa 1313
 DB 4089 ttatagaacacttaaaaaactaaagaa 4116
 RESULT 6
 AAQ78141

Db	303	atataatgtttatcatltaaggtgtgacccaatccttccatataatcatttaataatcaga	362
Qy	420	tgggtatcttcacagaataatgcgagggaatgatgtgtcttcgtataaatgaacaattgg	479
Db	363	gggagaataactcggaaatgacgagtcgatgttgatttttgatgatataagatttgg	422
Qy	480	atatacacaagaagggtttacaacgaggttgggtccaaattacataaatctggtccatc	539
Db	423	atataacacagaaggatcttccacaagaagatttgaccgtgatatacaaatccgatatactc	482
Qy	540	agtttaaatttaaggatgaataacgtcccaagaatgctatataatgtgaatgagtttaccg	599
Db	483	tgttccataatttgacacacaaaagtgctaatgatgttttaaaaaacatgagttgtaa	542
Qy	600	aaaaaagaataactaaaaaagtcaccaaaaaatggtgtttaaagtaagatttcttcaataa	659
Db	543	aaagcgtaataactaaaaaagtgtaagaanaaatgtaggttaaaagtgctcctttacacga	602
Qy	660	agaaataactattttcagatcatcttaatgtgaagatacacatcgagagataagaattttcga	719
Db	603	agagttaccataatttgccatttcgttgagagatacctcgtgaacctaaagattttgaga	662
Qy	720	tagaagagatagtttttaactataatcgatttgatcattttaagatagatgattagacc	779
Db	663	tagagaagatagtttttaataacaacgattccaacatttaagaacggtgttttagtacc	722
Qy	780	tctgcacataataaaatttgatgataatcttgaagaacttcaggaacttcagagactcga	839
Db	723	actagccataataactttgtatgagatataaggaacttaataatgaagaagaattggtc	782
Qy	840	aaataaagacttaaacagaagtcctaaagaatcttgaanaacgcacagatacaaaaaagc	899
Db	783	taataaagatataataaagctttaaagaacttggagaagcgcagagataataaaaaagc	842
Qy	900	acaaaataaaaaataaatttagacacagccaattaaagaacatgagcgaataatttgta	959
Db	843	acataacacaaaagaagaattttagacacacactcgatgcaatcagcaaaaataatga	902
Qy	960	agcaacaacaactcaattagaacacttgtaagcaattacgaattacacatctcgcggattcttc	1019
Db	903	agctaaacacttaaacagaagacatggtcaatgcaatccactctcgcggcttcttat	962
Qy	1020	tatttaacccttggaaagtgtgatacttaatgcaagttggaagtcgaataaataagaacct	1079
Db	963	aacttaaccggttggaaagtgttactacgcttggtagaactccaatcgttatgcgcatct	1022
Qy	1080	cgcctgaaagtatgcagttcaatgagactatgataatataatgcaattgatacgtgattga	1139
Db	1023	tgcagggagctacggttccaatggaagatgattactatgaaatcgaacatgaaatggtat	1082
Qy	1140	cogttataatttaaggagatttaagcgttcttttaacagatgctctcaaatgcaggtgt	1199
Db	1083	tctgataataattctatgagttatcattgagtgagactttagtgaagtgctgcaaga	1142
Qy	1200	tgtaaactttaaaaaagatttaatgcagatgtaaatgataatgttgttgattcgttaa	1259
Db	1143	agttaaagtttaaaaaggcctatgagtcgcgattgatatagaatcgttgttgacttttaa	1202
Qy	1260	acctataataaaccaatgtatcactatatacaacaacttaaaaaataaaaaa	1313
Db	1203	acctataataaaccaatgtataacatttatagacaacttaaaaaactaaagaa	1256
RESULT 7			
AAK37800			
ID	AAK37800 standard; DNA; 1295 BP.		
AC	AAK37800:		
XX	09-JUL-1999 (first entry)		
XX	Staphylococcus xylosus FemA DNA.		
XX			

[illegible]

DY Y

DY Y

DE Staphylococcus lugdunensis FemA DNA.
 XX FemA: identification; detection; therapy; infection; femB:
 KM amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX Staphylococcus lugdunensis.
 OS
 XX Key Location/Qualifiers
 FH 1..1280
 FT CDS /*tag- a
 FT /product= "FemA"
 FT /note= "partial sequence, no start or stop codon"
 PD MO9916780-A2.
 PN 08-APR-1999.
 XX 28-SEP-1998; 98MO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 XX MPI; 1999-287521/24.
 DR P-PSDB; AAY08216.
 XX New Staphylococcus-specific oligonucleotides
 PT Claim 17; Fig 7a-b; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 CC
 SQ Sequence 1280 BP; 484 A; 197 C; 221 G; 378 T; 0 other;

Query Match 58.6%; Score 787.6; DB 20; Length 1280;
 Best Local Similarity 77.4%; Pred. NO. 1.2e-123;
 Matches 955; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

QY 82 aaagctacgaattgctgcttttactgaaataatgcatatgacatttacaagatg 141
 DB 1 acagcaaatgaatcgggtgtttcacagatacaatgcatatgacatttaccatg 60
 QY 142 actgaataatgagtttaaaagtgtcgagaaactgaactcatttggtagaatt 201
 DB 61 acaggaactaatttaaaagtgtcgagaaactgaactcatttggtagaatt 120
 QY 202 aataaagaataagatgctgtgttctgtatgctaaactgtaccggttgaanaat 261
 DB 121 aataaagaataagatgctgtgttctgtatgctaaactgtaccggttgaanaat 180
 QY 262 tttaaatatttatacaaatcgtgtgcagatcattgattatgaatacaaaactgct 321
 DB 181 tttaaatatttatacaaatcgtgtgcagatcattgattatgaatacaaaactgct 240
 QY 322 caattttcttaacgaataagtaaatattttaaacaacaaactgtttatgtaagt 381

DB 241 caattttcttaacgaataagtaaatattttaaacaacaaactgtttatgtaagt 300
 QY 382 atagaccttatttgccttacaatcgtatcatatgtagtgaattacaggaatgct 441
 DB 301 atagaccttatttgccttacaatcgtatcatatgtagtgaattacaggaatgct 360
 QY 442 ggaatgattggttcttcgaataaagcaaatatgatatcaacaggaaggttaca 501
 DB 361 ggaatgattggttcttcgaataaagcaaatatgatatcaacaggaaggttaca 420
 QY 502 acagatttgcacataattacaatcgttccatcctcattttaaattaaagataaa 561
 DB 421 acagatttgcacataattacaatcgttccatcctcattttaaattaaagataaa 480
 QY 562 actgtaagaatgatttaaaagatgtagttagtgaanaaagaataactaaagatc 621
 DB 481 acagtaagaatgatttaaaagatgtagttagtgaanaaagaataactaaagatc 540
 QY 622 caaaaatggtgttaaaagatgtagttagtgaanaaagaataactaaagatc 681
 DB 541 tcaaaaatggtgttaaaagatgtagttagtgaanaaagaataactaaagatc 600
 QY 682 ttatggaagatcatcagagactaaagaatttctgtagagaggttagtttacct 741
 DB 601 ttatggaagatcatcagagactaaagaatttctgtagagaggttagtttacct 660
 QY 742 aatgatttcatctttaaagatgtagttagtgaanaaagaataactaaagatc 801
 DB 661 aatgatttcatctttaaagatgtagttagtgaanaaagaataactaaagatc 720
 QY 802 gatatcttgaagaacttcatcagagactaaagaatttctgtagagaggttagtttacct 861
 DB 721 gatatcttgaagaacttcatcagagactaaagaatttctgtagagaggttagtttacct 780
 QY 862 cttaaagatgtaaaagacagacatacaaaaagcacaataaataaataaattta 921
 DB 781 cttaaagatgtaaaagacagacatacaaaaagcacaataaataaataaattta 840
 QY 922 gaacgacttaaaagacagacatacaaaaagcacaataaataaataaattta 981
 DB 841 gaacgacttaaaagacagacatacaaaaagcacaataaataaataaattta 900
 QY 982 catgtaacgaattacacatcgtcgtgattcttctttaaataccttgaagttga 1041
 DB 901 catgtaacgaattacacatcgtcgtgattcttctttaaataccttgaagttga 960
 QY 1042 tattatgaggtgtagagctaaataatagacactcgtggaagtatgtagtcaa 1101
 DB 961 tattatgaggtgtagagctaaataatagacactcgtggaagtatgtagtcaa 1020
 QY 1102 tggactatgatttaataatgcaattgcatgcatgtagcgttataattttatgagatt 1161
 DB 1021 tggactatgatttaataatgcaattgcatgcatgtagcgttataattttatgagatt 1080
 QY 1162 agtgcattttaaagatgtagtgcagagatgtagtgcagagatgtagtgcagagatg 1221
 DB 1081 agtgcattttaaagatgtagtgcagagatgtagtgcagagatgtagtgcagagatg 1140
 QY 1222 aatgcagatgtagtgcagagatgtagtgcagagatgtagtgcagagatgtagtgcagagatg 1281
 DB 1141 aatgcagatgtagtgcagagatgtagtgcagagatgtagtgcagagatgtagtgcagagatg 1200
 QY 1282 tcaactatatacaacacttaaaaaataaaga 1315
 DB 1201 aaacttattcaggtttaaagaacttaaaata 1234

RESULT 9
 AAH52400
 ID AAH52400 standard; DNA; 1179 BP.
 XX
 AC AAH52400;

RESULT 12
AAX37803
ID AAX37803 standard; DNA; 1284 BP.
XX
AC AAX37803;

XX	Staphylococcus schleiferi FemA DNA.
DE	FemA; identification; detection; therapy; infection; femB;
XX	amplification; genotyping; gram-positive bacteria; vaccine; ss.
KW	Staphylococcus schleiferi.
OS	Staphylococcus schleiferi.
XX	
FF	Key Location/Qualifiers
FT	CDS 1..1297
FT	/tag= a "FemA"
FT	/product= "FemA"
XX	/note= "partial sequence, no start or stop codon"
XX	
PN	WO9916780-A2.
XX	
PD	08-APR-1999.
PF	28-SEP-1998; 98WO-BE00141.
XX	
PR	26-SEP-1997; 97EP-0870146.
PA	(BENA-) BELGIAN MIN NAT DEFENCE.
PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX	
PI	Gala J, Vannuffel P;
XX	
DR	WPI: 1999-287521/24.
DR	P-PSDB; AAY08219.
XX	
PT	New Staphylococcus-specific oligonucleotides
XX	
XX	Claim 23; Fig 10a-b; 48pp; English.
XX	This invention describes novel Staphylococcus-specific oligonucleotides
CC	based on the consensus femA nucleotide sequence which are used to
CC	develop products for the identification, detection and therapy of
CC	infections. The oligonucleotides can be used for the genetic
CC	amplification, the identification and/or quantification of various femA
CC	sequences which are specific to known or unknown Staphylococci species.
CC	Since the femA sequence is similar to the femB sequence, the
CC	oligonucleotides can also be used for the molecular genotyping of femB
CC	genes of different Staphylococci species or other gram-positive bacteria.
CC	The femA nucleic acid can also be used in therapeutic applications.
CC	They can also be used to identify inhibitors, e.g. antibodies or
CC	antisense oligonucleotides, for blocking expression of the femA
CC	nucleotide sequences. They can also be used for producing vaccines
CC	against Staphylococci infections.
XX	
SQ	Sequence 1297 BP; 495 A; 184 C; 249 G; 369 T; 0 other;
	Query Match 50.7%; Score 681; DB 20; Length 1297;
	Best Local Similarity 71.6%; Pred. No. 8.9e-106;
	Matches 894; Conservative 0; Mismatches 355; Indels 0; Gaps
QY	82 acggtacagaattggcgatctttactgaataaatgcataagccattttcacagatg 141
Db	1 acgagcgttgaaattggcgcttacagatcaaatgcataagccatttcacgcaatg 60
QY	142 actgaataattgatgtaaaagtctgcagaaaactgaaacctatttagaattaaa 201
Db	61 gtaggaactagaattaaagggtgctgaagggttggaaacacattctgcgcattcaa 120
QY	202 ataaagataataagtcattgctcttgttatgcttaactgctaccgcttatgaaatt 261
Db	121 gatacaacaataacgactagcagcatgtttactgacagcagtcgagtaagtatt 180
QY	262 tttaaattattttatcaaatctggtgccagtcattgattatgaaacaagaactcgtt 321
Db	181 tttaaattattttatcaaacccgaccagtcagtcagtaataaagaagtcgtt 240
QY	322 cactttttttaacgaattaagtaataattttaaaaaacaacattgtttatatgact 381

XX 09-JUL-1999 (first entry)
 XX Staphylococcus sciuri Fema DNA.
 DE Fema; identification: detection; therapy: infection; fema;
 KM amplification; genotyping; gram positive bacteria; vaccine; ss.
 XX Staphylococcus sciuri.
 OS
 XX Key Location/Qualifiers
 FT 1..1284
 FT /tag= a
 FT /product= "Fema"
 FT /note= "partial sequence, no start or stop codon"
 XX MO9916780-A2.
 XX 08-APR-1999.
 XX 28-SEP-1998; 98WO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MTN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB: AAI08220.
 XX New Staphylococcus-specific oligonucleotides
 PS Claim 25; Fig 11a-b; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the fema sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of fema
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 XX Sequence 1284 BP; 518 A; 181 C; 215 G; 370 T; 0 other;
 QY 91 gaattggcgattactgaataaaagccatagacatttaccagagatgaactgaat 150
 Db 7 gaattggaagcttttacaataaataatgcgacgagatttaccagacgtagtgaat 66
 QY 151 tatgagttaaagtgtgcgagaacgaacatttattgtaggaatataaataaagat 210
 Db 67 tatgattaaacacatcgtgaagttacttcaacacatttagtggggtcaagaataca 126
 QY 211 aatgaagtcattgtctgtgtatgtaactcgtaccggttaagaaatttttaaat 270
 Db 127 ggtgaagatttagctgcgtctgttaacaagtaccagttatggaagaatttattac 186
 QY 271 ttttttcaatcgtggtccagtcattgattagaataaagaactgttcaattttc 330
 Db 187 tttaactcaatagaggaccagtaagtattagcaacaagaactgttgcattttc 246

QY 331 ttaacgaattaaagtaattttaaaacaacacattgtttatgtacgtatagaccc 390
 Db 247 tttaagaatcgtgtgacattttaaagaatttaaaagatttcttctttagaacctc 306
 QY 391 tattgcttaataatcgttaacatgagatggtgatataacggagaatgctggagat 450
 Db 307 tacttgcacatacaactaagaatagatcatgagatatttataaaatcattcaacgt 366
 QY 451 tggttcttcgataaatgaaacaattagatatacaacgaagggtttacaagaagtt 510
 Db 367 ggtttaataacaacttgaacattgacattgattatgaacacaaagcttcaactgt 426
 QY 511 gatccattataactcgttccattcattcattttaaatttaagataaactgcgtaa 570
 Db 427 caccacatacctcaattagatggtcattcgttacttatttgaagatgagcgaaga 486
 QY 571 gatgattaaatggaatgtagtagtttaagaaaagaataactaaagctcaaaaat 630
 Db 487 acgctacatcaagaacatgacagatttaagaanaagaatacctaaagaagtcataa 546
 QY 631 ggtgttaagatgaatttcttactaagaagaatttactatttcagatcattatgaa 690
 Db 547 ggtttaaagttcgttttccattcaagaatggaatgacgattatccgtaattatgaa 606
 QY 691 gatactcagagactaaagaatttctgataagagagtagtttttaccatagattt 750
 Db 607 gatacagacagaagaagaatttccacagatcgtgagtagtacttaccatagata 666
 QY 751 gatactttaaagatagagatttagtagctctcgcattatataaattttagatatt 810
 Db 667 aaatctttgaaat---gtaagattcctttagacatataagacttgaacttaactt 723
 QY 811 gaagaacttcagcagaacgctgacacatttaataagacttaacaagaacttaagaat 870
 Db 724 ccaacattagaanaagaacacatgacacatcaacaagaatattgtgaagaagct 783
 QY 871 attgaanaagcagacatacaacaanaagcacaanaataaataattagacagca 930
 Db 784 ttgaanaagaacacagatatacaanaaagcatttaataatagacacatttaaca 843
 QY 931 ttaagaacaaatgagcaanaaattgtatgaagcacaacattcatttagagacatg 990
 Db 844 agagagaagaatgaagctaatattagaagaagcacttcaacttacaagaacatgtgt 903
 QY 991 gaattacaatacctcgtgatttcttcttatttattcaacttgaagttgatatgca 1050
 Db 904 acattaccaatagacagcgttcttcttatttattcaacttgaagttgatatgca 963
 QY 1051 ggtggaagcaataataatagacactcgttgaagttatgacgttcaatgactatg 1110
 Db 964 ggtgttcacatcgaatgaatatacgtcacttgcagtagtattgacattcagtggaag 1023
 QY 1111 attaatatgcaattgacatgacattgacacgttatattttagggatgagtgatc 1170
 Db 1024 attaatatgcaattgacatgacattgacacgttatattttagggatgagtgatc 1083
 QY 1171 tttaacagatgctgtgagatgaggtgtgttaaaatttaaaagatttaagatg 1230
 Db 1084 ttctcagaagaagacgtgactgtgtgtatttatttaaaagatttaagatg 1143
 QY 1231 gtaattgataatgtgtgtatttctttaaactataaactaaacaaatgattacatt 1290
 Db 1144 gttatgataatattgtgtatttctttaaactataaactaaacaaatgattacatt 1203
 QY 1291 acaacacttaaaaaatataaagaagat 1318
 Db 1204 acaacacttaaaaaatataaagaat 1231

583	ATGATAACGAAGTGAATGCCAGCTGTTTATTAACAGCTGTCTCTGTAAGAAATATTTA	524
266	aatatttttattcaaaacgtgggtccagtcattgattgaaaaacaaagactcgttcaact	325
523	AAATATTTTATTTCCCAATCGCGGCCAGTANTAGATTATATATTAAGAGCTGTGTACATT	464
326	ttttctttaaagaaataagtaaatattttaaacaacacacttgtttatatgtacgtatag	385
463	TTTTCTTTAATGAATGGATGAATATGATTAATAAATAATAATTCCTTTATATTTAAGAGTTG	404
386	accttatttgcttcatacatgatgtaacatgatgggtgatattacagaaaatgctggga	445
403	ACCCATACCTTCCATATCAATATTTAAATCATGAGGGAGAAATAACTGGAAATGCGAGTTC	344
446	atgatgtgtcttcataaaatgaacaataggatatacaacagaggggtttacaacag	505
343	ATGAATGGATTTTGTGAATTAGAGAGTTAGGATATTAACACGAAGGATCCACAAAG	284
506	gatttgatccaatattacaattcgggtccatcgttttaaatattaaaggataaaactg	565
283	GATTTGATCCTGATTACAAATCCGATCATCTGTTCTTAATTTAGCAAAACAAAGTG	224
566	ctaaagatgtattaaatgaatgatagttttaaagaaagaataactcaaaaaagtcctaaa	625
223	CTAATGATGTTTTTAAAAACATGGATGGTTTAAAGAACGTAATACTTAAAGAGTTAGA	164
626	aaaatggtgtaagaatgattcttctaagaagaataacctattttcagatcattta	685
163	AAATGGAGTTAAGTCCCGCTTTTATCTGAAGAGAGTTACCTATATTTAGTGCATTTA	104
686	tgaagatatacatcagagatcaagaataatttctgatagagagatagtttttactataatc	745
103	TGAGGATACCTCTGAACTAAAGATTTCAGATAGAGAAGATAGTTTTTATTACAACA	44
746	gatttgatcattttaagatagatagattagtaactctcgcata	788
43	GATTCAAACATTATAAGAGACCGTGTTTGTAGTACCAGTAGCCCTA	1
RESULT	14	
AAV74747/c		
ID	AAV74747 standard; DNA; 3271 BP.	
AC	AAV74747;	
CC		
XX	16-MAR-1999 (first entry)	
DT	Staphylococcus aureus contig SEQ ID #436.	
DE	Computer readable medium; vaccine; S.aureus infection; immunodetection;	
KW	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;	
KW	skin infection; surgical wound infection; scalded skin syndrome;	
KW	toxic shock syndrome; ds.	
XX	Staphylococcus aureus.	
OS		
XX		
PH	Key Location/Qualifiers	
FT	misc_feature 1561..1620	
FT	/*tag= a	
FT	/note= *these bases represent a line of missing text in	
FT	the sequence listing in the specification. They	
FT	are included to maintain the nucleotide numbering	
FT	given in the specification for this DNA sequence"	
XX		
PN	EP786519-A2.	
XX		
PD	30-JUL-1997.	
XX		
PF	07-JAN-1997; 97EP-0100117.	
XX		
PR	05-JAN-1996; 96US-0009861.	
PA	(HUMA-) HUMAN GENOME SCI INC.	

XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
 PI Rosen CA;
 XX WPI, 1997-374922/35.
 XX Polynucleotide(s) and proteins derived from *Staphylococcus aureus*
 PT stored on computer readable medium and used in the production of
 PT anti-*S.aureus* vaccines
 PS Claim 1; Page 1339-1340; 3271pp; English.
 XX This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the *S.aureus* DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against *S.aureus* infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC *S.aureus* in a sample. *S.aureus* is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the *S.aureus* DNA sequences contained on the
 CC computer readable medium.
 XX Sequence 3271 BP; 948 A; 625 C; 461 G; 1168 T; 69 other:
 SQ

Query Match 27.5%; Score 368.8; DB 18; Length 3271;
 Best Local Similarity 75.9%; Pred. No. 2,2e-53;
 Matches 492; Conservative 1; Mismatches 150; Indels 5; Gaps 3;

QY 3 aaatttaaatgaactcaataataaagaatcctaataattgagatagat 62
 DB 647 AAAAAGTCAATACGGAATGAATTAATTAACAGAGAGAAATAGGAGTAAAT--GAT 591
 QY 63 aatgaatttacaatttaaacagctacagaatttgcgatttactgcaaaaatgcata 122
 DB 590 AATGAGATTACAAATTAACAGCTTAAGAGTTGGTCCCTTACAGATGATGATGCA 531
 QY 123 tagcaatttacaagatgagatgaataatgatagtaaaagtctgagaaaatgaaac 182
 DB 530 CAGCAATTCACGCAACTGTTGCCCTATGAGTTAAAGCTGCTGTAAGATGTAAC 471
 QY 183 tcarttagtaggaatttaaaataaagaataagaatcagtcagtcgctgtgtgtgatacgc 242
 DB 470 ACATTTGTCGAGATTAATAAACAATTAACGAGGCTAGGAGCTTGCTTACTTCTC 411
 QY 243 tttaccgttatgaaaaatttttaataatttttaataatcgtgtgcagtcattgata 302
 DB 410 TGTACTGTATATAAGTGTTCAGATATTTTATTAATTCAGGCTGAGGATGATTA 351
 QY 303 tgaatacaaaagaaactgcttcaatttttcttaacgaattaaagaatttaaaaca 362
 DB 350 TGAATAATCAAGAACTGTCACCTTTTGTAAAGATTAATCAAAATATGTTAAAC 291
 QY 363 aactgtttatagtagatagacccttattgctcctatcaatctcgttaatacgtatg 422
 DB 290 TCGTGTCTATACCTACATATGATGATCCATATTAATCAATTAATCAATTAATCA 231
 QY 423 tgaattacagaaatgctggggaatgattgtttctcgataaataaacaattaggata 482
 DB 230 CGAGATTAACAGGATATGCTGTATATGATGCTCTTGTATTAATTAAGTAATTTG 171
 QY 483 tcaacagaagagtttacaacagatgatacacaatttaacaattcggttccactcagt 542
 DB 170 TGAACATTAAGATTCATTAAGATTTGATCTGCTCAAAATTCGATACACTCAGT 111

QY 543 ttaatttaaaagaaactgcttaagaatgtatataatgaaatgtagatg--ttacgaa 601
 DB 110 GTTAAATTTAAAGATTAAGAAAGCAGATGACATCAATTAATAATGATGACTTAAG 51
 QY 602 aaagaataactaaagaatgcacaaa--aaatggtgttaaaagaaattc 648
 DB 50 AANGAACACGAAAAAGTTAAAGAAAGATGCTTAAAGTAAAGTATT 3

RESULT 15
 AA074775
 ID AA074775 standard; DNA; 1251 BP.
 XX AA074775;
 AC 17-JUN-1995 (first entry)
 DT 17-JUN-1995 (first entry)
 XX Staphylococcus epidermidis fimb gene sequence.
 DE Staphylococcus epidermidis fimb gene sequence.
 XX Fimb; ds; methicillin-resistance; antibiotic.
 OS Staphylococcus epidermidis.
 XX Key Location/Qualifiers
 FH 1..1251
 FT CDS /*tag= a
 FT EP624650-A.
 XX 17-NOV-1994.
 PD 25-APR-1994; 94EP-0302949.
 XX 30-APR-1993; 93US-0057164.
 PR (ELIL) ELI LILLY & CO.
 PA Alborn Jr WE, Hoskins JA, Skatrud PJ;
 PI WPI, 1994-350790/44.
 DR P-PSDB; AAR67000.
 XX New fimb gene of *Staphylococcus epidermidis* - and related vectors,
 PT transformants and protein, for identifying active agents against
 PT methicillin-resistant *Staphylococcus*.
 PS Claim 2; Page 16-18; 23pp; English.
 XX The fimb gene encodes Fimb protein, a factor essential for
 CC methicillin-resistance. Gene disruption studies can be used with
 CC the aim of developing new antibiotics against methicillin-resistant
 CC *S. epidermidis*.
 XX Sequence 1251 BP; 468 A; 154 C; 230 G; 399 T; 0 other:
 SQ

Query Match 25.9%; Score 348.4; DB 15; Length 1251;
 Best Local Similarity 57.0%; Pred. No. 5.6e-50;
 Matches 722; Conservative 0; Mismatches 526; Indels 18; Gaps 4;

QY 64 atgaatttacaatttaacagatgaagaattggcgatttactgcaaaaatgcacat-- 121
 DB 1 atgaatttacaagagttacagatgaagaattgaaacttgcacaaatccatcacta 60
 QY 122 -atgcaatttacaacagatgactgcaaatattgttgtaaagttgtgagaactgaa 180
 DB 61 gaaagttattatccaaagtgaaagaaatgatgtacacgtgataagatggtgttaa 120
 QY 181 actcaatttagaaatttaaaataaagaataagaatgaatgcatgtgttactgaact 240
 DB 121 gtaagttatagtggttaaaagaacagacacataagatgtagcagcctgttct 180

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us-09-509-234c-52.rng

Fri Jun 21 08:38:29 2002

US-09-509-234C-52.rml

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 12:04:14 ; Search time 208.59 Seconds
(without alignments)
1581.503 Million cell updates/sec

Title: US-09-509-234C-52
Perfect score: 1343
Sequence: 1 taataatttaaatgacga.....taagaggggaatagtagaa 1343

Scoring table:
IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:
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2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	802.8	59.8	1257	1	US-08-330-154-1
2	278.8	20.8	453	3	US-08-714-918-9
3	278.8	20.8	453	4	US-09-265-315-9
4	278.8	20.8	453	4	US-09-265-315-9
5	278.8	20.8	453	4	US-09-266-417-9
6	251.2	18.7	410	3	US-08-714-918-6
7	251.2	18.7	410	4	US-09-265-315-6
8	251.2	18.7	410	4	US-09-266-417-6
9	251.2	18.7	410	4	US-08-714-918-4
10	232.4	17.3	400	4	US-09-265-315-4
11	232.4	17.3	400	4	US-09-265-315-4
12	232.4	17.3	400	4	US-09-265-315-4
13	232.4	17.3	400	4	US-09-266-417-4
14	103	7.7	5253	3	US-08-714-918-19
15	103	7.7	5253	4	US-09-265-315-19
16	103	7.7	5253	4	US-09-265-315-19
17	103	7.7	5253	4	US-09-266-417-19
18	76.4	5.1	19124	2	US-08-487-8268-13
19	68.4	4.9	19124	2	US-08-936-1658-74
20	65.2	4.9	19124	2	US-08-446-855A-1
21	63	4.7	8920	3	US-08-487-8268-13
22	63	4.7	8920	3	US-09-150-741-1
23	62.2	4.6	398	4	US-08-714-918-5
24	62.2	4.6	398	4	US-09-265-315-5
25	62.2	4.6	398	4	US-09-265-315-5
26	62.2	4.6	398	4	US-09-266-417-5
27	60	4.5	7218	1	US-08-232-463-14

28	59.4	4.4	240	1	US-08-628-417-6
29	59.4	4.4	2223	1	US-08-257-073-4
30	57.2	4.3	2447	2	US-09-014-969-14
31	56.8	4.2	3095	6	5231168-1
32	56.2	4.2	6243	2	US-09-056-075-1
33	55.8	4.2	658	4	US-08-998-416-595
34	55	4.1	5852	1	US-07-867-106-2
35	54.8	4.1	6124	4	US-08-713-419B-3
36	53.8	4.0	5361	4	US-08-973-462-2
37	53.6	4.0	1482	4	US-08-098-327E-41
38	52.8	3.9	4766	5	PCT-US93-07261-10
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42	52	3.9	1482	4	US-08-098-327E-45
43	52	3.9	1482	4	US-08-462-625-45
44	51.6	3.8	837	4	US-08-998-416-288
45					

ALIGNMENTS

RESULT 1
US-08-330-154-1
; Sequence 1, Application US/08330154
; Patent No. 5587307
; GENERAL INFORMATION:
; APPLICANT: Albhorn Jr., William E
; APPLICANT: Hoskins, Joann
; APPLICANT: Skatrud, Paul L
; APPLICANT: Unal, Serhat
; TITLE OF INVENTION: FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS,
; TITLE OF INVENTION: FEMA PROTEIN, AND VECTORS AND MICROORGANISMS COMPRISING
; TITLE OF INVENTION: THE FEMA GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Division/AEH
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330.154
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/208.925
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US/08/057.163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamilton, Amy E
; REGISTRATION NUMBER: 33,894
; REFERENCE/DOCKET NUMBER: X-8894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-1294
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

us-09-509-234c-52.rni

Fri Jun 21 08:38:29 2002

LOCATION: 1..1257
US-08-330-154-1

Query Match 59.8%; Score 802.8; DB 1; Length 1257;
Best Local Similarity 77.5%; Pred. No. 3.9e-156;
Matches 972; Conservative 0; Mismatches 282; Indels 0; Gaps 0;

QY 60 gataaagaatttcaaaattcaacagctacagaaatttgaggattttactgaaataatgcc 119
DB 3 GAAGATGAAGTTTACGAATTGACACCTPAAGATTAGTACTGATGATGAC 62
QY 120 atataccattttacacagactgaaattatgatgaaattgaaattgctgagaaactga 179
DB 63 ATATAGTCATTTACACAATGGAAGTAATTTACGAATTAAAGTTGCTGAAGGTACCGA 122
QY 180 aactcatttagtaggaataaaataaataaataaataaataaataaataaataaataa 239
DB 123 GTCACATTTAGTTGGAATTAATAATATGATACGAAGTATGCGACCTGTTTATTAAAC 182
QY 240 tctgtaccgttatgaaatttttaatttttttttttttttttttttttttttttttt 299
DB 183 ACCTGTTCCGTGTAAGTAATAATTTTAAATTTTATTTTCCAAATCGCGTCCAGTAATGA 242
QY 300 ttaataaacaagaactogttcacttttttttttttttttttttttttttttttttt 359
DB 243 TTAATAATAAAGAGCTGTACATTTTTCCTTAATGAATGAGTAATATGTAATAA 302
QY 360 acaacattgtttatagtcgtatagacccttttttttttttttttttttttttttttt 419
DB 303 ATATAATTTGTTTATTTAAGAGTTGACCAATACCTTCCATCATATTTAAATCATGA 362
QY 420 tgggtatattacaggaatgctgggaatgattggtttcttcgtataaataaataaataa 479
DB 363 GGGAGAAATTAACGTAATGACAGTCAATGATGATGATGATGATGATGATGATGATG 422
QY 480 atatacaacagaggttttacacaggtttgtatccaaatttcaaaattcgtttccattc 539
DB 423 ATATAACACGAGGATTTCCACAAAGGATTTGATGCTGTTTACAAATCCGATATCATTC 482
QY 540 agtttaatttaagataaagctaaagctaaagctaaagctaaagctaaagctaaagctaa 599
DB 483 TGTCTTAATTTAGCAACAAAGTCTAATGATGTTTAAATAAAGATGATGTTTAAAG 542
QY 600 aaaaagaataactaaaagctccaaaagctggttttaagtaagattttcttactaaaga 659
DB 543 AAACGCTATATCAAAAAGTTAAGAAATGGAATAATGAGTCCGCTTTTATCTGGAAGA 602
QY 660 agaattaccatttttcagatcatttgaagatacatcagagactaaagaattttcttga 719
DB 603 AGAGTTACCTATATTAGTTCATTTAGGAGGATACCTCTGAACCTAAAGATTTGCGAGA 662
QY 720 tagaagaatagtttttactataatcgattgatcatttttaagaatagatagtttagtacc 779
DB 663 TAGAGAAGATGAGTTTATTTATACAGATTTCAACATTTATAAGACCGTGTGTTAGTACC 722
QY 780 tctgcataataaaatttgatgaattcttgaagaacttcagacagctcagacatt 839
DB 723 ACTAGCTATATTAACTTTGATGATGATATATAGAGGAACTTAATTAAGAAATGTCGT 782
QY 840 aataaagacttaaaacagctcaaaagatttgaaacagcagcagatacaaaaaaagc 899
DB 783 TAATAAGATTATATAAAGCTTTTAAGACATTTGAGAACTGAGAACTCCAGAGAATAA 842
QY 900 acaaaataaaaaataaatttgaacagcagcaataaagaacaaatgcaaaataatgata 959
DB 843 ACATACAAAAAGGAATAATTTAGAACACAACTCGATGCAATACGAAAAAATAATGA 902
QY 960 agcaacaaactcaatagaacatggttaacgaattaccaaataatctgctgattctctt 1019
DB 903 AGCTAAACCTTAAACAAAGCAATGGAATTAATTTACCCATCTCTGCTGCTCTTTAT 962
QY 1020 tattaatccattggaattgtattattatgagggggaagctcaaaataaataatagacactt 1079

DB 963 AATTATCGGTTGAAGTACTTTACTACGCTGGGAACCTCAAAATCGTTATCGCCATTT 1022
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DB 1023 TGCAGGGAGCTATGCGGTTCAATGGAAGATGATTAATGCAATTTGAACATGTTATTA 1082
QY 1140 cccttataatttttgggatttagtggctattttacagatgactgctgaagatgcagggt 1199
DB 1083 TCGGTATAATTTCTATGTTATTTAGTGGTACCTTTAGTGAAGATGCTGAAGATGCTGG 1142
QY 1200 tgaataatttaaaaagatttaaatgagatgagatgagatgagatgagatgagatgag 1259
DB 1143 AGTTAGTTTAAAGGCTATGATGCGGATGTTATAGAAATACGTTGGTGACTTTATTA 1202
QY 1260 accataataataacaaatgatttaccattatatacaacacttaaaaaataaaaaa 1313
DB 1203 ACCTATTAAATAACCAATGATATAAATTTATAGAACACTTAATAAACTAAAGAA 1256

RESULT 2

US-08-714-918-9
; Sequence 9, Application US/08714918
; Patent No. 6037123
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ying
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08714,918
; FILING DATE: September 13, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,796
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-714-918-9

...TTTGGGCCCCCTATATTTNCTATGGGTGTAGTGGT 421

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QY     1168 catttacagatgatgtcgaagtgcaggtgt 1199  
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DB      422 NAATTCNAGNAGTGCTGAAGACTGCTGGTGT 453  
  
RESULT          5  
US-09-266-417-9  
; Sequence 9, Application US/09266417  
; Patent No. 6228588  
; GENERAL INFORMATION:  
; APPLICANT: Benton, Bret  
; APPLICANT: Lee, Ving J.  
; APPLICANT: Malouin, Francois  
; APPLICANT: Martin, Patrick K.  
; APPLICANT: Schmid, Molly B.  
; APPLICANT: Sun, Donxu  
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
;   OF INTEREST TO THE TREATMENT OF STAPHYLOCOCCUS AUREUS  
; TITLE OF INVENTION: TARGET GENES  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/266,417  
; FILING DATE: March 9, 1999  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/714,918  
; FILING DATE: September 13, 1996  
; APPLICATION NUMBER: 60/009,102  
; FILING DATE: December 22, 1995  
; APPLICATION NUMBER: 60/003,798  
; FILING DATE: September 15, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 240/248  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEX: (213) 955-0440  
; FAX: (213) 489-1600  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-266-417-9
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Db	2 TTAAAATAATACAAAGACCGGTGCTGNAGTCCTTNAGCCTGATATCAACA	Best Local Similarity 74.6%;	Pred. No. 5.6e-49;	Ind
QY	808 cttgaagaacttcattgcagacgcgtcagacattaataaagaccttaaac	Mismatches 337;	Conservative 0;	Mismatches 115;

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NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: US/09/265,315
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-9

Query Match          20.8%; Score 278.8; DB 4; Length 453;
Best Local Similarity 74.6%; Pred.No. 5.6e-49;
Matches 337; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY      748   ttgacatttaagatgagtattgtacctctcgcatataaaaaatttgagaatat 807
DB       2   TTAATAATTTACAAGACCGCTGTGTTNAGTACCCTTNAGCGTATATCAACTTTAATGAATAT 61
QY      808   ctggaagacttcgcagaacgctcagaccatttaataagacttaaacaaagcctcaaaa 867
DB     62   ATTAAGAAGAACTAACGAAGAGCGTGATATTTTAATAAAGATTTTAATAAAGCGTTAAAG 121
QY      868   gatattgaaaaacgcagcatacaaaaaagcacaaaaataaaaaataaataggacag 927
DB    122   GATATTGAAAAACGGCTCGTGAATAATAAAAAGCACATAACAAGCGAGATAACTTACAACAA 181
QY     928   caattaagaacaaatggcagaaaaattgatgaagcacacaacttcaattagaacatggt 987
DB    182   CAACTTGATGCAAANTGASCAAAAGATTGANGACGTTAAACGCTCAAGANGANGANCATGGT 241
QY     988   aacgaattaccaatatotcgtgagttctcttttaattccattgaagttgtatttat 1047
DB    242   AATGNVTTTAACTATCTCTCTGTTTCTCCCTTTATCAATCCNTTGGNGITGTTTTATAT 301
QY    1048   gcaggtggaacgtccaataaataatagacacctcgctggaagttagcagttccaatggact 1107
DB    302   GCTGGTGGTAGCAACAAATGCNTTCGTCATTTTNCGGANGTGTATGCTGCAATGGGAA 361
QY    1108   atgattaattgcaattgatcatcgttgacgttaccgttataattttatgggattagtggt 1167

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1 INFORMATION FOR SEQ ID NO: 6:
2 SEQUENCE CHARACTERISTICS:
3     LENGTH: 410 base pairs
4     TYPE: nucleic acid
5     STRANDEDNESS: single
6     TOPOLOGY: linear
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8 US-08-714-918-6
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FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-6

Query Match 18.7%; Score 251.2; DB 4; Length 410;
 Best Local Similarity 75.4%; Pred. No. 2.4e-43;
 Matches 307; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
 QY 725 aggatagttttactataatcattgacattttaaagatagagattagtagctctcg 784
 Db 4 ATGACAAATNTAACTACATCGCTTAAATATTACAAAGACCGCTGTGTGACCTTTAG 63
 QY 785 catatataaaatttgatgaactcttggaactctcagaaagcagcagcattaaata 844
 Db 64 CGTATATCACTTTAATGATATATTAAGAACTTAACGAGAGCGGTGATATTTAAATA 123
 QY 845 aagacttaacaaagctctaaagattgaaaagcagcagcagcagcagcagcagcagc 904
 Db 124 AAGATTAAATTAAGCGTTAAAGGATATTGAAACCGTCTGAAATATAAAAGCAGATA 183
 QY 905 ataaaaataaatttagaagcagcagcagcagcagcagcagcagcagcagcagcagc 964
 Db 184 ACAAGCGAGATTAATTAACAACTTTGATGCAATGAGCAATGAGCAATGAGCAATG 243
 QY 965 cacaacttaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1024
 Db 244 AAGCTTCAAGAGACATGTTGATGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 303
 QY 1025 atccattgaagttgattattatgcaggtggaagcagcagcagcagcagcagcagcagc 1084
 Db 304 ATCCATTGANGTTGTTTATTATGCTGGTGTACATCAATGCAATGCAATGCAATG 363
 QY 1085 gaagttatgcagttcaatgagcattgattaaattgcaattgcat 1131
 Db 364 GAAGTTATGCTGCAATGGAATGATTAAATGATGCAATGCAATGCAATGCAATG 410

RESULT 8
 US-09-265-315-6
 Sequence 6, Application US/09265315
 Patent No. 6187541
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ying J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: TARGET GENES

NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 SUITE: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-6

Query Match 18.7%; Score 251.2; DB 4; Length 410;
 Best Local Similarity 75.4%; Pred. No. 2.4e-43;
 Matches 307; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
 QY 725 aggatagttttactataatcattgacattttaaagatagagattagtagctctcg 784
 Db 4 ATGACAAATNTAACTACATCGCTTAAATATTACAAAGACCGCTGTGTGACCTTTAG 63
 QY 785 catatataaaatttgatgaactcttggaactctcagaaagcagcagcattaaata 844
 Db 64 CGTATATCACTTTAATGATATATTAAGAACTTAACGAGAGCGGTGATATTTAAATA 123
 QY 845 aagacttaacaaagctctaaagattgaaaagcagcagcagcagcagcagcagcagc 904
 Db 124 AAGATTAAATTAAGCGTTAAAGGATATTGAAACCGTCTGAAATATAAAAGCAGATA 183
 QY 905 ataaaaataaatttagaagcagcagcagcagcagcagcagcagcagcagcagcagc 964
 Db 184 ACAAGCGAGATTAATTAACAACTTTGATGCAATGAGCAATGAGCAATGAGCAATG 243
 QY 965 cacaacttaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1024
 Db 244 AAGCTTCAAGAGACATGTTGATGCAATGAGCAATGAGCAATGAGCAATGAGCAAT 303
 QY 1025 atccattgaagttgattattatgcaggtggaagcagcagcagcagcagcagcagcagc 1084
 Db 304 ATCCATTGANGTTGTTTATTATGCTGGTGTACATCAATGCAATGCAATGCAATG 363
 QY 1085 gaagttatgcagttcaatgagcattgattaaattgcaattgcat 1131

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Fri Jun 21 08:38:29 2002

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Wardburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 240/247

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-4

Query Match 17.3%; Score 232.4; DB 4; Length 400;

Best Local Similarity 74.5%; Pred. No. 1.7e-39;

Matches 298; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 286 ggtccagtcattgattatgaacacacgaagactgcttcttcttcaacgaatta-ag 344

Db 400 GTCCAGTGATTGANTATGAAATCAAGNACTCGTACACTTTTCTTTATGATTATCC 341

QY 345 taatattataaacacacacattttatgtacgtatagaccccttatttgccttaca 404

Db 340 AAAATATGTTAAAAACATCGTGTGCTATACCTACATCAGATCCATATTACCATCA 281

QY 405 atactgtaactgattgattatgaacacacgaagactgcttcttcttcaacgaatta 464

Db 280 ATACTGTGATCATGATGGCGAGATTACAGGTAAATGCTGTGTAATGATTGGTCTTTGATAA 221

QY 465 aatgaacacattaggatatacaacgaagactgcttcttcttcaacgaatta 524

Db 220 ATAGTAACTTAGGATTGAAACATACCTGATTCATTAAGGATTGCTGTGCTACA 161

QY 525 aattcggtccattcagtttttaaaatttaaaagataaaaactgcttaagatgtattcaatgg 584

Db 160 AATCGGTTATCAGTCAGTGTGATTAAAGATATAAAGATATAAAGATATAAAGATATAAAG 101

QY 585 aatgtagattttacgaaaaaagaataactataaaagctcccaaaaagctggtttaaagtaag 644

Db 100 TAGGATGAGCTTAGAAAAAGAAACACGGAANNAGTTNAAAAGATGGTGTAAAGTAAG 41

QY 645 atttttactaaagaataactatttctcagatcattt 684

Db 40 ATTTTATCTGAAGGAGNACTACCAATTTTATAGATTATT 1

RESULT 11

US-09-265-315-4/c

; Sequence 4, Application US/09265315

; Patent No. 6187541

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/265,315

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

Query Match 17.3%; Score 232.4; DB 3; Length 400;

Best Local Similarity 74.5%; Pred. No. 1.7e-39;

Matches 298; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

QY 286 ggtccagtcattgattatgaacacacgaagactgcttcttcttcaacgaatta-ag 344

Db 400 GTCCAGTGATTGANTATGAAATCAAGNACTCGTACACTTTTCTTTATGATTATCC 341

QY 345 taatattataaacacacacattttatgtacgtatagaccccttatttgccttaca 404

Db 340 AAAATATGTTAAAAACATCGTGTGCTATACCTACATCAGATCCATATTACCATCA 281

QY 405 atactgtaactgattgattatgaacacacgaagactgcttcttcttcaacgaatta 464

Db 280 ATACTGTGATCATGATGGCGAGATTACAGGTAAATGCTGTGTAATGATTGGTCTTTGATAA 221

QY 465 aatgaacacattaggatatacaacgaagactgcttcttcttcaacgaatta 524

Db 220 ATAGTAACTTAGGATTGAAACATACCTGATTCATTAAGGATTGCTGTGCTACA 161

QY 525 aattcggtccattcagtttttaaaatttaaaagataaaaactgcttaagatgtattcaatgg 584

Db 160 AATCGGTTATCAGTCAGTGTGATTAAAGATATAAAGATATAAAGATATAAAGATATAAAG 101

QY 585 aatgtagattttacgaaaaaagaataactataaaagctcccaaaaagctggtttaaagtaag 644

Db 100 TAGGATGAGCTTAGAAAAAGAAACACGGAANNAGTTNAAAAGATGGTGTAAAGTAAG 41

QY 645 atttttactaaagaataactatttctcagatcattt 684

Db 40 ATTTTATCTGAAGGAGNACTACCAATTTTATAGATTATT 1

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Page 9

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-4

Query Match 17.3%; Score 232.4; DB 4; Length 400;
Best Local Similarity 74.5%; Pred. No. 1.7e-39;
Matches 298; Conservative 0; Mismatches 101; Indels 1; Gaps 1;
QY 286 ggtccagtcattgtatgaagaacagagctcttcttcttaagaatta-ag 344
DB 400 GGTCCAGTCATTGTATGAAGAACAGAGCTCTTCTTCTTAAGATTATCC 341
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DB 340 AAAATGTGTTAAAAAACATGCTGTTGCTATACCTACATACATTCATCA 281
QY 405 atatcgaatcagtgatgattacaggaagatgctggatgattgcttgcataa 464
DB 280 ATACTGGAATCATGATGCGAGATTACAGTATGCTGTTATGATGCTCTTCA 221
QY 465 aatgaacaattagatatcaacaacgaaggttacaacagagattgacaaatata 524
DB 220 AATGAGTAACCTTAGATTGAACTACTGATTCATTAAGGATTTGATCTGTCTCA 161
QY 525 aattcgcttccattcagtttaaatcttaagaataaactgcttaagaatgataag 584
DB 160 AATCGGTATACCTAGCTAGTTAGATTAAAGATTAAGATGACATCTTAAAA 101
QY 585 aatgagagtttaccgaagaagaataactaagaagaatccaaanaaatggtttaaag 644
DB 100 TATGATGAGACTTAGAAAAAGAAACACGGAANNAGATTAAAGATGTTAAAGTAAG 41
QY 645 attcttactaagaagaattaccatttccagatcatt 684
DB 40 ATTATTATCTGAAGAGNACTACATTTTAAATTTT 1

RESULT 13
US-09-266-417-4/c
Sequence 4, Application US/09266417
Patent No. 6228588
GENERAL INFORMATION.

APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmidt, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-4

Query Match 17.3%; Score 232.4; DB 4; Length 400;
Best Local Similarity 74.5%; Pred. No. 1.7e-39;
Matches 298; Conservative 0; Mismatches 101; Indels 1; Gaps 1;
QY 286 ggtccagtcattgtatgaagaacagagctcttcttcttaagaatta-ag 344
DB 400 GGTCCAGTCATTGTATGAAGAACAGAGCTCTTCTTCTTAAGATTATCC 341
QY 345 taatatataaacaacacatggttataatgtagtagacccttattgcttaca 404
DB 340 AAAATGTGTTAAAAAACATGCTGTTGCTATACCTACATACATTCATCA 281
QY 405 atatcgaatcagtgatgattacaggaagatgctggatgattgcttgcataa 464
DB 280 ATACTGGAATCATGATGCGAGATTACAGTATGCTGTTATGATGCTCTTCA 221
QY 465 aatgaacaattagatatcaacaacgaaggttacaacagagattgacaaatata 524
DB 220 AATGAGTAACCTTAGATTGAACTACTGATTCATTAAGGATTTGATCTGTCTCA 161
QY 525 aattcgcttccattcagtttaaatcttaagaataaactgcttaagaatgataag 584

us-09-509-234c-52.rni

Fri Jun 21 08:38:29 2002

517 atttacaattcggttcattcagttttaaatttaaaggataaaactgctctaaagatga 576
 2907 GACTTACATCCAAACCCAGTATGACTATGTTACACCAATTTGATAAAATGATGATGAGTTA 2848
 577 ttaattggaattgagtagtttcagaaaaaagaaatactaaataaagtcctaaataatggtgt 636
 2847 TTAATAGTTTGAACGCGGAAATCGTTCAAAAAGTGCCTGGCTTTAAAGCAGGATCG 2788
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 2787 ACAGTAGAACGATCTGATAGAGAGGTTTAAACACATTTGCTGAGCTTAATGAAATCACT 2728
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 871 attgaaaaacgacagataac-----aaaaagcacaataaaaaataaatttagaacag 927
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 928 caattaaaagcaaatgagcaaaaattgatgaagcaacacacactcaattagaacatggt 987
 2487 AAAATGCTAAAAATGAAGATTTAAACGAGACCTAGAGCTTTAGAAAAGGAAACATCCT 2428
 988 aacgaattaccaatctcgtggtattcttcttatttaataccattggaattgatatat 1047
 2427 GAAGGTATTTATCTTTCGTTGCTGACTATTAATGCTTGTGCTGCTCAAAATCATATTTACTTA 2368
 1048 gcaggtggaacgtcaataataatagacacttcgctggaagttatgagttcaatgagat 1107
 2367 TATGCTGCTTCTTAATGAATTTAGAGATTTTTCACCAATCATATGACGATATAGC 2308
 1108 atgattaatatgaattatcatgctgacattgacgcttataattttttagggattgaggt 1167
 2307 ATGATGAAGTATGACGCTGAACATGCTGCAACAACTTACGATTTGCGGTGACAGATAT 2248
 1168 cattttacagatgctgagatgaggtggttgaataatttaaaaaagatttaagca 1227
 2247 GATCCAGATAAGACTCAGAACATTTATGGATTTATGGGCATTTAAAAAGTGTGGGAACA 2188
 1228 gatgtaattgaattggtggttcgttaaacctataataaaccacattgatttaccata 1287
 2187 TACTTAAGTGAAGATTTGGTGAATTTGATTTGATTTGAATCAGCCATTTGTRCCAATTA 2128
 1288 tataaacacttaaa 1302
 2127 ATTGACCAAGTTAAA 2113

RESULT 15
 US-09-265-315-19/c
 ; Sequence 19, Application US/09265315
 ; Patent No. 6187541
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Ving J.
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 ; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 ; TITLE OF INVENTION: TARGET GENES
 ; NUMBER OF SEQUENCES: 111

160 AATCCGTTATCACTCAGTGTAGTTTAAAGATAAAACAGCAGATGACATCATNAAA 101
 585 aatgtagattttacgaaaaaagaaatactataaagtcctaaataatggttttaagtaag 644
 100 TAIGGATGACTTACAAAAGAAACACGGAANNAGTTNAAAGAAATGTTTAAAGTAAG 41
 645 atttctactaaagaagaattaccatttttcagatcattt 684
 40 ATTTTATCTGAGGAGNACTACCAATTTTATGATTTT 1

RESULT 14
 US-08-714-918-19/c
 ; Sequence 19, Application US/08714918
 ; Patent No. 6037123
 ; GENERAL INFORMATION:
 ; APPLICANT: Benton, Bret
 ; APPLICANT: Lee, Ving
 ; APPLICANT: Malouin, Francois
 ; APPLICANT: Martin, Patrick K.
 ; APPLICANT: Schmid, Molly B.
 ; APPLICANT: Sun, Dongxu
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 ; TITLE OF INVENTION: TARGET GENES
 ; NUMBER OF SEQUENCES: 111
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/714,918
 ; FILING DATE: September 13, 1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION NUMBER: 60/009,102
 ; FILING DATE: December 22, 1995
 ; APPLICATION NUMBER: 60/003,798
 ; FILING DATE: September 15, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 222/005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5253 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-714-918-19

Query Match 7.7%; Score 103; DB 3; Length 5253;
 Best Local Similarity 46.7%; Pred. No. 9e-13;
 Matches 399; Conservative 1; Mismatches 446; Indels 9; Gaps 2;
 Qy 457 ttcgataaaatgaacattagatatacaacagaggttttacaacagatttgatcca 516
 2967 TTGCAAAATTTGAAGCGCTTGGTTTTAAACATTAAGGATTTAAGAGGTTTATCAAAA 2908

Fri Jun 21 08:38:29 2002

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Page 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO.: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-19

Query Match 7.7%; Score 103; DB 4; Length 5253;
Best Local Similarity 46.7%; Pred. No. 9e-13;
Matches 399; Conservative 1; Mismatches 446; Indels 9; Gaps 2;
QY 457 ttcgataaagaacacataagatatacaacgaagggttaacaagagattgaccca 516
DB 2967 ttgcataaatttgaaagcgcttgctttaacataaagattttaaagagtttatcaaaa 2908
QY 517 atattacaattcggttcacatcagttttaatttaagataaaactgctaagaatgta 576
DB 2907 gactacatccaacacacgtatgactatgatttacacccaattgataaaatgatgatgta 2848
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DB 2847 ttaaaatgatttgaaagcgcaaaatcgcttcaaaagtcgctttaaagcgagtagc 2788
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QY 928 caattaagaacaaatgagcaaaaaattgtagaagcaacacacttcaattagaacatgct 987
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QY 988 aacgaattacaatcctgctgalttcttactaataccattggaagttgatttact 1047
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DB 2247 gatccagataaaagcctgaaacattttagattatggcattttaaagctggcggaaca 2188
QY 1228 gatgtaattgaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1287
DB 2187 tacttgaagtaaaagattggaatttgaatttgaatttgaatttgaatttgaatttgaattt 2128
QY 1288 tatacaacacttaaa 1302
DB 2127 attgacgaattttaa 2113

Search completed: June 20, 2002, 12:04:20
Job time: 20975 sec

us-09-509-234c-52.rni

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Fri Jun 21 08:38:31 2002

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:27:04 ; Search time 8551.36 Seconds
(Without alignments)
2119.711 Million cell updates/sec

Title: US-09-509-234C-52
1343
Sequence: 1 taaatttaataatagtcac.....taagaggggaatgtagaag 1343

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em.estba:*
2: em.esthum:*
3: em.estinu:*
4: em.estinu:*
5: em.estov:*
6: em.estpl:*
7: em.estro:*
8: em.estc:*
9: gb.est1:*
10: gb.est2:*
11: gb.htc:*
12: gb.gss:*
13: em.gss.hum:*
14: em.gss.inu:*
15: em.gss.pln:*
16: em.gss.vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98.4	7.3	1025	12	CNS014J2
2	95	7.1	769	12	AG134867 Pan trogl
3	93.4	7.0	781	12	CNS009PO
4	93.2	6.9	879	12	CNS01JRG
5	91.4	6.8	1101	12	CNS01J2H
6	90.4	6.7	614	12	CNS0152H
7	89.2	6.6	1101	12	BE420745
8	89.2	6.6	1101	12	CNS00L72
9	88.4	6.5	1135	12	CNS0336Q
10	87.4	6.5	1059	12	CNS0022B
11	87.2	6.5	619	9	AL514935
12	87.2	6.5	1092	12	CNS020K7
13	86.8	6.5	737	12	CNS008B0
14	86.2	6.4	747	12	CNS011R0
15	86.2	6.4	974	12	CNS0017T
16	85.8	6.4	1101	12	CNS00EVL
17	85.8	6.4	1101	12	CNS01219

C 18	85.2	6.3	1101	12	CNS001EB	AL1060733	Drosophila
C 19	85.2	6.3	1101	12	CNS01V2	AL1085536	Drosophila
C 20	85	6.3	652	12	CNS03HOU	AL244551	Tetradodon
C 21	84.6	6.3	1029	12	CNS01ZGM	AL174271	Tetradodon
C 22	84.6	6.3	1198	12	B08337	B08337	T199-Sp. 1
C 23	84.4	6.3	928	12	CNS00DNK	AL071865	Drosophila
C 24	83.6	6.2	871	12	A2671726	A2671726	ENTM0505TE
C 25	83.6	6.2	908	12	A2548467	A2548467	ENTMEX30TR
C 26	83.4	6.2	716	12	CNS03VOB	AL262448	Tetradodon
C 27	83.4	6.2	796	9	AL524807	AL524807	
C 28	83.2	6.2	891	12	CNS009JU	AL053767	Drosophila
C 29	83.2	6.2	1042	12	CNS014RK	AL103838	Drosophila
C 30	83	6.2	984	12	CNS03ANQ	AL252575	Tetradodon
C 31	83	6.2	990	12	CNS006OI	AL065624	Drosophila
C 32	82.8	6.2	922	12	A2548363	A2548363	ENTM207FE
C 33	82.8	6.2	924	10	BK415947	BK415947	OP21029 M
C 34	82.8	6.2	1101	12	CNS0153V	AL104565	Drosophila
C 35	82.4	6.1	1020	12	CNS0038G	AL228940	Tetradodon
C 36	82.4	6.1	1101	12	CNS00396	AL323578	Tetradodon
C 37	82.4	6.1	1101	12	CNS00396	AL063921	Drosophila
C 38	82.2	6.1	910	10	BK415636	BK415636	OP20714 M
C 39	81.8	6.1	886	12	CNS055DF	AL249961	clone BAO
C 40	81.8	6.1	788	3	B1645011	B1645011	OP2810 M
C 41	81.8	6.1	981	12	CNS002BD	AL189701	Tetradodon
C 42	81.8	6.1	1185	10	B2727407	B2727407	GA-EP001
C 43	81.6	6.1	982	12	AQ257599	AQ257599	nbx00021B
C 44	81.6	6.1	1036	12	CNS00599	AL057797	Drosophila
C 45	81	6.0	738	12	A2195503	A2195503	SP_1030_A

ALIGNMENTS

RESULT 1
LOCUS CNS014J2/c
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
BACN11111 of Drosophila library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL104216
VERSION 1
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM BACN11111 of Drosophila
REFERENCE 1 (bases 1 to 1025)
AUTHORS Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
TITLE Genoscope.
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT
- Web : www.genoscope.cns.fr
- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CNRS (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
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1. 1025
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone-lib="DrosBAC"
/clone="BACN11111"
/note="end : 77"
BASE COUNT 148 a 88 c 6 g 522 t 261 others
ORIGIN

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AG134867
AG134867.1 GI:16664545
GSS: GSS (genome survey sequence), clone_lib:PTB Chimpanzee Male
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-147P14.F.

ORGANISM
Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of library PTB

REFERENCE
2 (bases 1 to 769)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. 769
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-147P14.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 521 a 28 c 24 g 78 t 118 others
ORIGIN

Query Match 7.18; Score 95; DB 12; Length 769;
Best Local Similarity 45.4%; Pred. No. 0.00094;
Matches 244; Conservative 0; Mismatches 293; Indels 1; Gaps 1;

QY 464 aaatgaacaaataggatatacaacacgaggtttacacagaggttgatccatattac 523
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Db 147 AAATAAATTGNAATTAANAAANAAANAAANNAATAGNNAAGNNGAATTNAAATAAANA 206
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QY 524 aaatcggttccattcagtttttaaatgaaggaataaaactgctaaagatgtatataatg 583
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Db 207 TNAANNANANANNNNAATANNATNAAANAAATGAAANAAANAAANAAANAAANAA 266
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QY 644 gattcttactaagaagattacattacattttcagatcatttgcagagatcagag- 702
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Db 327 AATTTTTTATNATTAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAAAN 386
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QY 703 actaagaattttctgtagagaggtatttttactataatcgtattgattcattttaa 762
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Db 387 AANNAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAA 446
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QY 763 gatagagatttagtacctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 822
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Db 447 AAAAAAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAAANAA 506
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QY 823 gcagaacgctgagacatttaataaagacttaacacagctctaaagacttaagacgaa 882
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Query Match 7.3%; Score 98.4; DB 12; Length 1025;
Best Local Similarity 35.0%; Pred. No. 0.00031;
Matches 322; Conservative 106; Mismatches 489; Indels 2; Gaps 1;

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Db 1015 DAKKAAAAAANAAAAAANAAAAAAGGTTAAATTAANAAATTAANAAATTAANAAATTA 956
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QY 214 gaagtcattgctgttatgctaaactgctgaccgttatgaaatttttaataatttt 273
|||||
Db 955 TATGTTTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 896
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QY 274 tattcaaatcggttccagtcattgattatgaacaaagaaactgctcactttttttt 333
|||||
Db 895 GTAKTTTGGDRADAAAAGGTGTGATWAGRAAAATTTTWTATTAATTTGATGATGAT 836
|||||
QY 334 aagcaaatgaatgaatatttaaaacaaacaaactgtttattatgtacgtatgacccctat 393
|||||
Db 835 RWAANAAAAAAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAG 776
|||||
QY 394 ttgcttataatcgttaactatgctggtgatattacaggaatgctgggaatgattgg 453
|||||
Db 775 AAAAAKTTTGTGTGTAANAAATATGTTGTATWATTAATTTTWTATTAATTTGATGAT 716
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QY 454 ttctcgataaaatgaacaaataggatatacaacacgaggtttacacagaggtttgat 513
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Db 715 AWANAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 658
|||||
QY 514 ccaattatacaaatgctgttcattcagtttttaatttaaaaggataaaactgctaaagt 573
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Db 657 KKAITTTGAATGTTTGTGKAWAAAAAANAAANAAANAAANAAANAAANAAANAAANAA 598
|||||
QY 574 gtataaatgaatgattgatttcagaaagaaataactcaaaagtcacaaagtcacaaagtc 633
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Db 597 WTKTTTAAWAAGKGGTGGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAG 538
|||||
QY 634 gttaaatgaatgttttactaagaagaattacatttccatttccagatcatttgaagat 693
|||||
Db 537 GAADAAKAGDAARADAGWAANAAARAKRTATATGTTGTTKTKTGTAGTAAGAKTAA 478
|||||
QY 694 acatcagagactaagaattttctgtagagaggtatttttactataatcgtattgat 753
|||||
Db 477 TWAAAGTTGTAKAWATTAATTAANAAANAAANAAANAAANAAANAAANAAANAAANAA 418
|||||
QY 754 catttaagaatagatttagtacctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 813
|||||
Db 417 KKTAAANAAAAATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 358
|||||
QY 814 gaacttcagacagcgcagacatttaataaagacttaaaagacttaaaagacttaaaagact 873
|||||
Db 357 AAAAAAANANANANANANANANANANANANANANANANANANANANANANANANANAN 298
|||||
QY 874 gaaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 933
|||||
Db 297 AAAAAAANANANANANANANANANANANANANANANANANANANANANANANANANAN 238
|||||
QY 934 aagcaaatgacaaatgattgagcaacacacacacacacacacacacacacacacacacac 993
|||||
Db 237 AAAAAAANANANANANANANANANANANANANANANANANANANANANANANANANAN 178
|||||
QY 994 ttaccaatctgctggatttcttatttaattcatttgaattgatttatttatttatttatt 1053
|||||
Db 177 ANNANANANANANANANANANANANANANANANANANANANANANANANANANANAN 118
|||||
QY 1054 gaaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1072
|||||
Db 117 TTHCNCNCAATCTTTA 99
|||||

RESULT 2
AG134867 769 bp DNA linear GSS 04-NOV-2001
LOCUS AG134867
DEFINITION Pan troglodytes DNA, clone: PTB-147P14.F, genomic survey sequence.

```

Db 507 TAAA 566

Qy 883 ccagatacaaaaagcacaaataaataattgacagcaacttaagcaaat 942

Db 567 AATTTAAANNNGAAAAAAAAAAAAAAAAANNTTANACCAAAATAAAAAAAAAA 626

Qy 943 gagcaaaaattgacgacacacacttaattgacacgacgtaacgaattaccaa 1000

Db 627 ACAGAAAAAAAAAAAAAAAAAAAAAAAAAGNATAAATTAATAAAAAAAAA 684

RESULT 3

CNS009D0 781 bp DNA linear GSS 03-JUN-1999

LOCUS Drosophila melanogaster genome survey sequence TE13 end of BAC #

DEFINITION BACR19009 of RPCL-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.

ACCESSION AL053444.1 GI:4934889

VERSION AL053444.1

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 781)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr

- determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pierer de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source 1..781

location/Qualifiers

1..781

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="RPCL-98"

/clone="BACR19009"

/note="end : TE13"

BASE COUNT 440 a 71 c 6 g 189 t 75 others

ORIGIN

Query Match 7.0%; Score 93.4; DB 12; Length 781;

Best Local Similarity 45.7%; Pred. No. 0.0015;

Matches 226; Conservative 22; Mismatches 247; Indels 0; Gaps 0;

Qy 536 atcagtttaaatgaagataaactgctaaagtatttaataagtagagtagt 595

Db 49 WTAAATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTA 108

Qy 596 tacgaaaaagaatacacaagaagtcacaaaagaatggttaagaatttacta 655

Db 109 TNAATATWMAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAAATTA 168

Qy 656 aagaagaattaccatttcagatcatttgaagaatatacagagactaagaattt 715

Db 169 AATTAAT 228

Qy 716 ctgacagagagatagtttactataatcgattgcatcttttaagaatagatag 775

Db 229 ATAAATTAATAAAAMATTAATTAATTAATTAATTAATTAATTAATTAATTA 288

Qy 776 taccctgcacataataattgacgatalctggaagacttcagagaactcaga 835

Db 289 AATTTAAAAATTTAAAAATTAATAAAATTAATAAAATTAATAAAATTAATAAA 348

Qy 836 catlaataaagaacttaacaaagcctaagaatattgaaaaagcagaatacaaa 895

Db 349 AAAAAAAAAAAAAAAAAAMATTAATTAATTAATTAATTAATTAATTAATTAATTA 408

Qy 896 aagcaaaaataaaaaataattagaacgaactaaagaacaatgagcaaaaattg 955

Db 409 AAAAAAAAAAMTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 468

Qy 956 atgaagacacacacttaactaataagatgtaagaaattcaatctcgtcgtctt 1015

Db 469 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 528

Qy 1016 tcttataatccat 1030

Db 529 AATTAATTAATAAAAT 543

RESULT 4

CNS01JRG 879 bp DNA linear GSS 12-JUN-2001

LOCUS Anopheles gambiae GSS T7 end of clone 14D07 of NotreDame1 library

DEFINITION from strain PST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.

ACCESSION AL147405.1 GI:7005551

VERSION AL147405.1

KEYWORDS GSS.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.

REFERENCE 1 (bases 1 to 879)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr

- 2 (bases 1 to 879)

- Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

- Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France

- This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES

source 1..879

location/Qualifiers

1..879

/organism="Anopheles gambiae"

/strain="PST"

/db_xref="taxon:7165"

/clone="14D07"

/clone_lib="NotreDame1"

/note="end : T7"

BASE COUNT 66 a 38 c 1 g 670 t 104 others

ORIGIN

Query Match 6.9%; Score 93.2; DB 12; Length 879;

Best Local Similarity 41.3%; Pred. No. 0.0016;

Matches 278; Conservative 53; Mismatches 341; Indels 1; Gaps 1;

Qy 331 tttaacgaattaagtaattatttaaacacacacattgttatatgacgtatagacct 390

Db 855 TATATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAGTAGTAATTAATTAATTAATTA 796

[illegible]

QY	Db	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898
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QY 1250 attcgtataa 1260
 Db 728 TKKDKKAAWA 738

RESULT 9
 CDS033GQ 1135 bp DNA Linear GSS 15-MAY-2000
 LOCUS Tetradon nigroviridis genome survey sequence PUC-Or1 end of clone
 DEFINITION 208P24 of library G from Tetradon nigroviridis, genomic survey
 sequence.

ACCESSION AL226115
 VERSION AL226115.1 GI:7885026
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetradon nigroviridis.
 ORGANISM Tetradon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 1135)
 AUTHORS Roest-Crolius H., Jallion O., Dasilva C., Fizames C., Fisher C.,
 Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and
 Weissenbach J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigroviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1135)
 AUTHORS Roest-Crolius H., Jallion O., Dasilva C., Bouneau L., Fisher C.,
 Bernot A., Fizames C., Winkler P., Brottier P., Quetier F.,
 Saurin W. and Weissenbach J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetradon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1135)
 AUTHORS Direct Submission
 TITLE Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 JOURNAL This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetradon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetradon.
 FEATURES
 source Location/Qualifiers
 1..1135
 /organism="Tetradon nigroviridis"
 /db_xref="taxon:99883"
 /clone_id="208P24"
 /clone_1id="G"
 /note="Genoscope sequence ID : C0AG208DH12SP1-end :
 PUC-Or1"

BASE COUNT 863 a 65 c 43 g 124 t 40 others
 ORIGIN

Query Match 6.6%; Score 88.4; DB 12; Length 1135;
 Best Local Similarity 46.3%; Pred. No. 0.0061;
 Matches 251; Conservative 9; Mismatches 282; Indels 0; Gaps 0;

QY 461 atcaaatcaacattggtatcaacacgaagggttacaacaggattgaccat 520
 Db 369 AA 428
 QY 521 tacaattcggtccattcagtttaatttaaggataaactgtaagatgataa 580
 Db 429 AA 488
 QY 581 atggaatgattgattcgaagaagaatactcaaaagtcacaaatggtgtaag 640
 Db 489 AA 548
 QY 641 taagattcttactaagaagaattccatttcagatcattatggaagatatacag 700
 Db 549 AAAAAAAAAATATTAATAAAAAAAAAAAAAAAAAAAAAAAAAATTAATAA 608

QY 701 agactaagaatttcgatagagagatagttttctataatcattgatactta 760
 Db 609 AA 668
 QY 761 aagatagatttagtaccctcgcacatatataaattgataatcttgaagaattc 820
 Db 669 AATATTTAAA 728
 QY 821 atcgagaacgtcagacattaaataagacttaacaaagctcctaagaatgaaac 880
 Db 729 AAAAAAAAAATATCAATNTAAAAAAAAAAAAAAAAAAAAAAAAAA 788
 QY 881 gaccagatacaaaaagcacaaaataaataattagacagcaattaaagca 940
 Db 789 AATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 848
 QY 941 atgagcaaaaattgataagcacacacttaattgaacatgtaacgattaccaa 1000
 Db 849 AAATCAATTA 908
 QY 1001 ta 1002
 Db 909 AA 910

RESULT 10
 CDS0022B/C 1059 bp DNA Linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence 17 end of BAC
 DEFINITION BACN01115 of Drosophila library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL097133
 VERSION AL097133.1 GI:5608744
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1059)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
 - Determination of this BAC-end sequence was carried out as part of a
 collaboration of this BAC-end sequence was carried out as part of a
 library (Dros BAC) was made by Alain Billaut at CPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.
 FEATURES
 source Location/Qualifiers
 1..1059
 /organism="Drosophila melanogaster"
 /plasmid="pBelobAC11"
 /db_xref="taxon:7227"
 /clone_1id="DrosBAC"
 /clone="BACN01115"
 /note="end : 17"

BASE COUNT 14 a 21 c 66 g 760 t 198 others
 ORIGIN

Query Match 6.5%; Score 87.4; DB 12; Length 1059;
 Best Local Similarity 40.0%; Pred. No. 0.0084;
 Matches 286; Conservative 44; Mismatches 385; Indels 0; Gaps 0;

QY 288 tccagtcattgattgaaacaaagaactcgcttcatttccttaagatataagtaa 347
 Db 757 KCAKSCMKRBRBCKRCWACAYAAACKSCBAKCKCAAAKMANAAAAAAAA 698

Fri Jun 21 08:38:31 2002

/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"

BASE COUNT 52 a 8 c 10 g 514 t 35 others

ORIGIN

Query Match 6.5%; Score 87.2; DB 9; Length 619;

Best Local Similarity 45.2%; Pred. No. 0.011;

Matches 245; Conservative 3; Mismatches 294; Indels 0; Gaps 0;

QY 461 ataaatgaacaattaggatatacaacgaagggtttacaacagagattgatccaatat 520
 Db 575 AA 516
 QY 521 tacaatttcggttcattcattttaaatttaaaagataaaactgctaaagatgattaa 580
 Db 515 AA 456
 QY 581 atggaatgagatgtttacgaagaaatactaaagtcacaaagtcacaaagtcacaa 640
 Db 455 AA 396
 QY 641 taagatttcattacaaagaagaatttaccatttttcagatcatttatggaagatacag 700
 Db 395 AA 336
 QY 701 agactaaagaatttcgtgagagagatgttttactataatcgatgattgatttata 760
 Db 335 AA 276
 QY 761 aagataagatttagtacctcgcataataaaatttgatgaatatttgagaagacttc 820
 Db 275 NNN 216
 QY 821 atgcgaacgtcagacatttaataaagacttaacaaagctctaaagatattgaaaac 880
 Db 215 AA 156
 QY 881 gaccagatacaaaaaagcacaataaaaaataaatttagacagcaatttaaaagcaa 940
 Db 155 AA 96
 QY 941 atgagcaaaattgatgagcaacacacttcaattagacatggttaacgaattacca 1000
 Db 95 AA 36
 QY 1001 ta 1002
 Db 35 AA 34

RESULT 12

CNS020K7

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence T7 end of clone

222111 of library G from Tetraodon nigroviridis, genomic survey

sequence.

AL175696

ALI75696.1

GI:7813753

GSS; genome survey sequence.

KEYWORDS

Tetraodon nigroviridis.

SOURCE

ORGANISM

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;

QY 348 atatttaaacacaacattgtttatgtacgtatagacaccttattgcttatacata 407
 Db 697 AAAAAAAAAAAKAKKKKKDAKKWAAAKKAAKAAADGKAKAAATDKKKNKKKAAK 638
 QY 408 tcgtaaatcattggtgtattacaggaatgctgggaatgattggttcttcgataaa 467
 Db 637 ATGRDAKADDAKAKAAAAAADRGAATAAAKAAKAGDAAGKGTGATGKGDAA 578
 QY 468 gaacaattaggatatacaacgaagggtttacaacagagatttgatccaattataca 527
 Db 577 AA 518
 QY 528 tcggttcattcattttaaatttaaaaggttaaaactgctaaagatgtattaaatga 587
 Db 517 AA 458
 QY 588 ggaattttacgaagaagaatactaaaggtccaaagtcacaaagtcacaaagtcacaa 647
 Db 457 AA 398
 QY 648 tcttactaaagaagaatttaccattttcagatcattttggaagatacatcagagactaa 707
 Db 397 AA 338
 QY 708 agaattttcgtgagagagatgttttttactataatcgatgattgatttataagatag 767
 Db 337 AA 278
 QY 768 agtattgacctcgcataataaaatttgatgaatatttcgagaacttcacaga 827
 Db 277 AA 218
 QY 828 acgtcagacattaaagaacttaacaaagctctaaagatattgaaagacagaccaga 887
 Db 217 AA 158
 QY 888 taacaaagaacacaaataaaataatttagaacagcaatttaaaagcaaatgagca 947
 Db 157 AA 98
 QY 948 aaaaattgatgagcaacacacttcaattagacatggtgacgaattacacata 1002
 Db 97 AA 43

RESULT 11

AL514935/c 619 bp mRNA linear EST 13-FEB-2001

LOCUS AL514935 LTI_NFL006_PL2 Homo sapiens cDNA clone CLOBB012D08 3

DEFINITION prime, mRNA sequence.

AL514935

AL514935.1

GI:12778428

EST.

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 619)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRI cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..619

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CLOBB012D08"

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FEATURES

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CNS008BU/c

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Ddb			470 CAKCAKAKCAAATTKCACTATTKMTMKKKAKTAYRTACAAMWAKANAKATAYACB	529
Qy			1080 cgtcggaagttgatcgactgaagggactatgattaattatgcaattgcatgagcattga	1139
Ddb			530 AKKAGBAKAKAKCKWKCKBKTKMCKCKCKYABACMKCCACBKTYNGINTGHACKA	589
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Ddb			650 KKKNTVYTAKTAKKAKKAAKTNAKBBBMHAAKMTGBKCKCKMNHNNDMMVKMK	709
Qy			1260 acta 1264	
Ddb			710 ACKNA 714	
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LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

EcocRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp; the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. 974

Location/Qualifiers

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/db_xref="taxon:7227"

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BASE COUNT

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Best Local Similarity 38.44; Pred. No. 0.012;

Matches 208; Conservative 65; Mismatches 269; Indels 0; Gaps 0;

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DB 104 NA 103
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Search completed: June 20, 2002, 14:27:12
Job time: 17742 sec

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11	14.4	28.8	20	6	A97448	A97448 Sequence 4
12	14.2	28.4	36	6	AX000930	AX000930 Sequence
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14	14.2	28.4	31	6	AX048724	AX048724 Sequence
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31	13.2	26.4	36	3	CENOMYFR	AR107709 Sequence
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33	13	26.0	22	6	AR175179	AR175179 Sequence
34	13	26.0	30	6	I46763	I46763 Sequence 5
35	13	26.0	35	6	I43351	I43351 Sequence 5
36	13	26.0	48	6	I25926	I25926 Sequence 6
37	13	26.0	50	6	I09118	I09118 Sequence 4
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44	12.8	25.6	24	6	AX036387	AX036387 Sequence
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58	12.8	25.6	24	6	AX036517	AX036517 Sequence
59	12.8	25.6	24	6	AX036524	AX036524 Sequence
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132922 Sequence 9
 142199 Sequence 12
 173519 Sequence 9
 AR028247 Sequence
 AR138650 Sequence
 AR169896 Sequence
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 AR115846 Sequence
 AR248516 Sequence
 AR249171 Sequence
 AR304627 Sequence
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 BD002595 Gene comp
 BD008391 A method
 137240 Sequence 25
 194090 Sequence 25
 U34617 Gallus gall
 A14998 Nucleotide
 A14999 Nucleotide
 A18333 oligonucleo
 A92751 Sequence 5
 AR001133 Sequence
 AX000896 Sequence
 AX045471 Sequence
 BD010744 Helicobac
 A00695 Artificial
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 AR055005 Sequence
 AR142302 Sequence
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 AX116607 Sequence
 AX343178 Sequence
 AX343182 Sequence
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 BD008385 A method
 BD011026 HIV probe
 E37844 Process for
 I00406 Sequence 28
 I00409 Sequence 31
 I27175 Sequence 30
 I32756 Sequence 30
 I46884 Sequence 30
 I84690 Sequence 30
 AR108960 Sequence
 AX236522 Sequence
 I40360 Sequence 5
 AX107591 Sequence
 C75695 Homo sapien
 C75705 Homo sapien

ALIGNMENTS

RESULT 1
 LOCUS A97446 35 bp DNA linear PAT 26-JAN-2000
 DEFINITION Sequence 2 from Patent WO9916780.
 ACCESSION A97446
 VERSION A97446.1 GI:6780792
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 35)
 AUTHORS Gala, J. and Vannuffel, P.
 TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
 JOURNAL Patent: WO 9916780-A 2 08-APR-1999;
 FEATURES GALA JEAN LUC (BE); UNIV LOUVAIN (BE) Location/Qualifiers

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 Db 1 ANRATGAATTACNAATTTCACGNCNANAGANTT 35
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 LOCUS AR079211 40 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 10 from patent US 5965426.
 ACCESSION AR079211
 VERSION AR079211.1 GI:10005957
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS Sakai, Y., Kato, N. and Shibano, Y.
 TITLE Protein disulfide isomerase gene derived from strain of methylotrophic yeast
 JOURNAL Patent: US 5965426-A 10 12-OCT-1999;
 FEATURES Location/Qualifiers
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 LOCUS E16040 40 bp DNA linear PAT 28-JUL-1999
 DEFINITION PCR primer for inserting Not I site to protein disulfide isomerase gene.
 ACCESSION E16040
 VERSION E16040.1 GI:5710723
 KEYWORDS JP 1998127294-A/4.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS Sakai, Y., Kato, N. and Shibano, Y.
 TITLE PROTEIN DISULFIDE ISOMERASE GENE DERIVED FROM METHANOL YEAST
 JOURNAL Patent: JP 1998127294-A 4 19-MAY-1998;
 COMMENT OS None
 OC Artificial sequences.
 PN JP 1998127294-A/4
 PD 19-MAY-1998
 PF 20-AUG-1997 JP 1997237822
 PR 04-SEP-1996 JP 96P 234287
 PI SAKAI YASUYOSHI, KATO NOBUO, SHIBANO YUJI
 PC C12N15/09, C07K14/39, C12N1/19, C12N9/90, (C12N15/09, C12R1:72), PC (C12N1/19, C12R1:72), (C12N9/90, C12R1:72);

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Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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AX162446/c 50 bp DNA linear PAT 22-JUN-2001
LOCUS AX162446
DEFINITION Sequence 5774 from Patent W00140521.
ACCESSION AX162446
VERSION AX162446.1 GI:14543777
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5774 07-JUN-2001;
Curagen Corporation (US)
LOCATION/Qualifiers
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Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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LOCUS AX162448
DEFINITION Sequence 5776 from Patent W00140521.
ACCESSION AX162448
VERSION AX162448.1 GI:14543779
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5776 07-JUN-2001;
Curagen Corporation (US)
LOCATION/Qualifiers
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Query Match 30.8%; Score 15.4; DB 6; Length 50;
Best Local Similarity 59.4%; Pred. No. 3.7e+05;
Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 16 aatgaattacnaatttgaacngcnaagant 47
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Db 40 AATGAACCTTAAGACTTTTCACGACGATGAGT 9

RESULT 7
EL3173/c 37 bp DNA linear PAT 24-JUN-1998
LOCUS EL3173
DEFINITION PCR primer.
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TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

JOURNAL
Patent: WO 9916780-A 4 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)

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/db_xref="taxon:32644"

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Db 2 AATGAAGTTACNAATT 19

RESULT 12
LOCUS AX000930 36 bp DNA linear PAT 10-MAR-2000
DEFINITION Sequence 3 from Patent WO9902989.
ACCESSION AX000930
VERSION AX000930.1 GI:7241174

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE
1 (bases 1 to 36)
AUTHORS Fersht, A. and Chatellier, J.

TITLE CHAPERONE FRAGMENTS
JOURNAL Patent: WO 9902989-A 3 21-JAN-1999;
MEDICAL RES COUNCIL (GB); FERSHT ALAN (GB)

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Db 34 GAATTTACGCTTACCTGCCATA 10

RESULT 13
LOCUS AX048695 36 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 9 from Patent WO0069907.
ACCESSION AX048695
VERSION AX048695.1 GI:12225850

KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE
1 (bases 1 to 36)
AUTHORS Hill, F.C., Chatellier, J. and Fersht, A.M.
TITLE Protein scaffold and its use to multimerise monomeric polypeptides
JOURNAL Patent: WO 0069907-A 9 23-NOV-2000;
MEDICAL RESEARCH COUNCIL (GB)

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Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 34 GAATTTACGCTTACCTGCCATA 10

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DEFINITION Sequence 9 from Patent WO0069886.
ACCESSION AX048724
VERSION AX048724.1 GI:12225869

KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE
1 (bases 1 to 36)
AUTHORS Hill, F.C., Chatellier, J. and Fersht, A.M.
TITLE Oligomeric chaperone proteins
JOURNAL Patent: WO 0069886-A 9 23-NOV-2000;
MEDICAL RESEARCH COUNCIL (GB)

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BASE COUNT
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Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 19 gaattacnaattacnagcnaa 43
Db 34 GAATTTACGCTTACCTGCCATA 10

RESULT 15
LOCUS AX248640 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 719 from Patent WO0166800.
ACCESSION AX248640
VERSION AX248640.1 GI:15863263

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 31)
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 719 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

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/db_xref="taxon:9606"

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Query Match
Best Local Similarity 28.0%; Score 14; DB 6; Length 31;
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Fri Jun 21 08:38:15 2002

Qy 19 gaattttacnaatttna 35
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Db 31 GAATTTTACCAATTYA 15

Search completed: June 20, 2002, 23:42:07
Job time: 17352 sec

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235	12	24.0	25	19	AAV58847	PCR primer ADJ027.
236	12	24.0	25	19	AAV58848	PCR primer ADJ028.
237	12	24.0	25	19	AAV58849	Gravule bound star
238	12	24.0	25	19	AAV58850	Human immunodefici
239	12	24.0	25	19	AAV58851	HIV amplification pr
240	12	24.0	25	19	AAV58852	Human immunodefici
241	12	24.0	25	19	AAV58853	PDI promoter 140 f
242	12	24.0	25	19	AAV58854	Human pax protein
243	12	24.0	25	19	AAV58855	Nesleria species
244	12	24.0	25	19	AAV58856	3' PCR primer OT-1
245	12	24.0	25	19	AAV58857	Nucleotide sequenc
246	12	24.0	25	19	AAV58858	Probe based on B.b
247	12	24.0	25	19	AAV58859	B. burgdorferi PC-
248	12	24.0	25	19	AAV58860	CTA475 Synthetic c
249	12	24.0	25	19	AAV58861	A. thaliana ribofl
250	12	24.0	25	19	AAV58862	(-)-limonene-6-hyd
251	12	24.0	25	19	AAV58863	A. thaliana ribofl
252	12	24.0	25	19	AAV58864	Spearmint (-)-limo
253	12	24.0	25	19	AAV58865	Left side amplifia
254	12	24.0	25	19	AAV58866	Nucleotide sequenc
255	12	24.0	25	19	AAV58867	HIV gag amplifia
256	12	24.0	25	19	AAV58868	S.pombe pho4 gene
257	12	24.0	25	19	AAV58869	Escherichia coli D
258	12	24.0	25	19	AAV58870	Staphylococcus aur
259	12	24.0	25	19	AAV58871	Human map-related
260	12	24.0	25	19	AAV58872	Human map-related
261	12	24.0	25	19	AAV58873	Human map-related
262	12	24.0	25	19	AAV58874	Human map-related
263	12	24.0	25	19	AAV58875	Human map-related
264	12	24.0	25	19	AAV58876	Human map-related
265	12	24.0	25	19	AAV58877	Human map-related
266	12	24.0	25	19	AAV58878	Human map-related
267	12	24.0	25	19	AAV58879	Human map-related
268	12	24.0	25	19	AAV58880	Human map-related
269	12	24.0	25	19	AAV58881	Human map-related
270	12	24.0	25	19	AAV58882	Human map-related
271	12	24.0	25	19	AAV58883	Human map-related
272	12	24.0	25	19	AAV58884	Human map-related
273	12	24.0	25	19	AAV58885	Human map-related
274	12	24.0	25	19	AAV58886	Human map-related
275	12	24.0	25	19	AAV58887	Human map-related
276	12	24.0	25	19	AAV58888	Human map-related
277	12	24.0	25	19	AAV58889	Human map-related
278	12	24.0	25	19	AAV58890	Human map-related
279	12	24.0	25	19	AAV58891	Human map-related
280	12	24.0	25	19	AAV58892	Human map-related
281	12	24.0	25	19	AAV58893	Human map-related
282	12	24.0	25	19	AAV58894	Human map-related
283	12	24.0	25	19	AAV58895	Human map-related
284	12	24.0	25	19	AAV58896	Human map-related
285	12	24.0	25	19	AAV58897	Human map-related
286	12	24.0	25	19	AAV58898	Human map-related
287	12	24.0	25	19	AAV58899	Human map-related
288	12	24.0	25	19	AAV58900	Human map-related
289	12	24.0	25	19	AAV58901	Human map-related
290	12	24.0	25	19	AAV58902	Human map-related
291	12	24.0	25	19	AAV58903	Human map-related
292	12	24.0	25	19	AAV58904	Human map-related
293	12	24.0	25	19	AAV58905	Human map-related
294	12	24.0	25	19	AAV58906	Human map-related
295	12	24.0	25	19	AAV58907	Human map-related
296	12	24.0	25	19	AAV58908	Human map-related
297	12	24.0	25	19	AAV58909	Human map-related
298	12	24.0	25	19	AAV58910	Human map-related
299	12	24.0	25	19	AAV58911	Human map-related
300	12	24.0	25	19	AAV58912	Human map-related
301	12	24.0	25	19	AAV58913	Human map-related

us-09-509-234c-1_copy_1_50.primer.rng

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959 10.8 21.6 27 20 AAX87837 Phosphatidylglycer
c 960 10.8 21.6 27 22 AAX39954 SNP specific lower
c 961 10.8 21.6 28 16 AAX92590 Thermus thermophil
c 962 10.8 21.6 28 18 AAT94764 Human progesterone
c 963 10.8 21.6 28 18 AAT84755 Primer for human P
c 964 10.8 21.6 29 15 AAV71897 LO-CD2a Vb RACE-PC
c 965 10.8 21.6 29 19 AAV57436 Staphylococcus aur
c 966 10.8 21.6 29 19 AAV62616 LO-CD2a chimeric a
c 967 10.8 21.6 29 19 AAV38779 PCR primer used to
c 968 10.8 21.6 29 19 AAV22872 PCR primer for Gre
c 969 10.8 21.6 29 20 AAX31639 PCR primer for Gre
c 970 10.8 21.6 29 20 AAX31640 PCR primer used to
c 971 10.8 21.6 29 20 AAX1041 Hammerhead ribozym
c 972 10.8 21.6 29 21 AAF05852 E. coli heterologo
c 973 10.8 21.6 30 16 AAT04765 5' primer for 56RB
c 974 10.8 21.6 30 17 AAT04779 E. coli chloramphen
c 975 10.8 21.6 30 18 AAT48103 Petunia flower bud
c 976 10.8 21.6 30 19 AAV44906 Arabidopsis Mlo fu
c 977 10.8 21.6 30 20 AAZ30432 Plasmid pGRXhNP P
c 978 10.8 21.6 30 21 AAA99149 HI loop region PCR
c 979 10.8 21.6 30 21 AAX07497 Bacteriophage Mu R
c 980 10.8 21.6 30 22 AAD21278 PCR primer H76041-
c 981 10.8 21.6 30 22 AAF24606 Human L-TM-alpha
c 982 10.8 21.6 30 24 AAD26324 Primer to amplify
c 983 10.8 21.6 31 15 AAV67530 Nucleotide fragmen
c 984 10.8 21.6 31 19 AAX06381 Human biallelic po
c 985 10.8 21.6 31 20 AAX64041 Green fluorescent
c 986 10.8 21.6 31 21 AAX97428 pea praz2 gene prom
c 987 10.8 21.6 31 21 AAX99145 Plasmid pGRShNP P
c 988 10.8 21.6 31 21 AAX39636 Vector pIC5:GFP PC
c 989 10.8 21.6 31 22 AAX30107 Human single nucle
c 990 10.8 21.6 31 22 AAX30762 Staphylococcus aur
c 991 10.8 21.6 32 20 AAX21084 Oligonucleotide RB
c 992 10.8 21.6 32 20 AAX55481 CGRP receptor gene
c 993 10.8 21.6 33 17 AAT08717 Human vesicular tr
c 994 10.8 21.6 33 22 AAT6841 Mitotic kinase ASK
c 995 10.8 21.6 33 24 ABA03721 Human Cdk5 related
c 996 10.8 21.6 33 24 ABA04099 Human Cdk5 related
c 997 10.8 21.6 33 24 ABA04100 Nucleotide sequenc
c 998 10.8 21.6 34 19 AAV36566 PCR primer used in
c 999 10.8 21.6 34 22 AAF30966

ALIGNMENTS

RESULT 1
AAX37751
ID AAX37751 standard; DNA; 35 BP.
XX
AC AAX37751;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 1.
XX
KW femA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
OS Staphylococcus sp.
XX
PN WO9916780-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-BE00141.
XX
PR 26-SEP-1997; 97EP-0870146.
XX
PA (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.

XX Gala J, Vannuffel P;
PI WPI; 1999-287521/24.
XX
DR New Staphylococcus-specific oligonucleotides
XX
PT Claim 5; Page 8; 48pp; English.
XX
PS This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the femA sequence is similar to the femA sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.
XX
SQ Sequence 35 BP; 12 A; 3 C; 3 G; 9 T; 8 other;
Query Match 54.0%; Score 27; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 anaatgaatttcaaattnacngcanagantt 48
|||||
Db 1 anaatgaatttcaaattnacngcanagantt 35
RESULT 2
AAX37792/C
ID AAX37792 standard; DNA; 29 BP.
XX
AC AAX37792;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 27.
XX
KW femA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
OS Staphylococcus sp.
XX
PN WO9916780-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-BE00141.
XX
PR 26-SEP-1997; 97EP-0870146.
XX
PA (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI Gala J, Vannuffel P;
PI WPI; 1999-287521/24.
XX
PD New Staphylococcus-specific oligonucleotides
XX
PF Example 1; Fig 1; 48pp; English.
XX
PS This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
CC

CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various feta
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the feta sequence is similar to the feta sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of feta
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The feta nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the feta
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 CC
 CC Sequence 29 BP; 8 A; 5 C; 2 G; 14 T; 0 other;

Query Match 34.4%; Score 17.2; DB 20; Length 29;
 Best Local Similarity 67.9%; Pred. No. 5.7e+02;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 18 tgaattacnaattacnagana 45
 DB 29 TGAATTACAGAGTTAACGTTAAGCA 2

RESULT 3

AAV22803
 ID AAV22803 standard; DNA; 40 BP.

XX AAV22803;

XX 24-JUN-1998 (first entry)

DE PCR primer used to amplify the PDI of *Candida boidinii*.

XX Protein disulphide isomerase; PDI; methylothrophic yeast;

KW *Candida boidinii* strain S2; endoplasmic reticulum; stable conformation;

KW recombinant; disulphide bond; secretory protein; gene therapy;

KW endoplasmic reticulum retention signal sequence; genetic

XX engineering; PCR primer; ss.

XX Synthetic.

XX *Candida boidinii*.

XX EP828004-A2.

XX 11-MAR-1998.

XX 04-SEP-1997; 97EP-0306871.

XX 04-SEP-1996; 96JP-0234287.

XX (SUNR) SUNTORY LTD.

XX Kato N, Sakai Y, Shibano Y;

XX WPI; 1998-161102/15.

XX Methylothrophic yeast protein di:disulphide isomerase - and

XX corresponding gene useful for increasing yields of secreted

XX heterologous proteins in *Candida boidinii*

XX Example 2; Page 6; 30pp; English.

XX PCR primers AAV22803-04 were used to amplify the protein disulphide

XX Isomerase (PDI) derived from *Candida boidinii* and to create NotI

XX sites at both ends of the DNA sequence. PDI is a major protein

XX present in the lumen of the endoplasmic reticulum. PDI is believed

XX to be an enzyme which catalyses formation of stable conformation by

XX recombining disulphide bonds of secretory proteins. As the protein

XX must stay in the endoplasmic reticulum, it has a sequence known as

XX the endoplasmic reticulum retention signal sequence at the carboxy

XX terminus (AAW56317) The PDI protein is useful in gene therapy and

CC genetic engineering. The PDI gene may be coexpressed with a gene of
 CC interest to ensure the production of a correctly folded biologically
 CC active protein.
 CC
 CC Sequence 40 BP; 18 A; 6 C; 7 G; 9 T; 0 other;

Query Match 32.8%; Score 16.4; DB 19; Length 40;
 Best Local Similarity 77.3%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 14 aaatgaantacnaattna 35
 DB 17 aaatgaagttaactta 38

RESULT 4

AAI78833/C
 ID AAI78833 standard; DNA; 50 BP.

XX AAI78833;

XX 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid seq:5774.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000NO-US32758.

XX 30-NOV-1999; 99US-0168138.

XX 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy -

XX Claim 1; Page 2277; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide

XX sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AAI73114 to AAI75329 represent peptides related to human polymorphic

XX polynucleotide sequences. The sequences can be used in gene and protein

XX therapy, and in vaccine production. (I) and the polypeptides encoded by

XX them may be used in the prevention, diagnosis and treatment of diseases

XX associated with inappropriate expression of polymorphic polypeptides.

XX For example, (I) may be used to treat disorders by rectifying mutations

XX or deletions in a patient's genome that affect the activity of

XX polypeptides by expressing inactive proteins or to supplement the

XX patients own production of polypeptide. Additionally, (I) and its

XX complementary sequences may also be used as DNA probes in diagnostic

XX assays to detect and quantitate the presence of similar nucleic acids

XX in samples, and therefore which patients may be in need of restorative

XX therapy. The polypeptides encoded by (I) may be used as antigens in the

XX production of antibodies specific for polymorphic polypeptides. The

XX antibodies may also be used to down regulate expression and activity

XX of the antibodies may also be used as diagnostic agents for detecting the

XX presence of polymorphic polypeptides in samples.

XX Sequence 50 BP; 16 A; 7 C; 7 G; 20 T; 0 other;

* us-09-509-234c-l_copy_l_50.primer.rng

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QY 16 aatgaatttcaaattnacnagant 47
 ||||| | | | | | | | | | | | | | | | |
 Db 41 AATGAACCTAAAGACTTTTCACAGCAGATGAGT 10

Query Match 30.8%; Score 15.4; DB 22; Length 50;
 Best Local Similarity 59.4%; Pred. No. 3.1e+03;
 Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 16 aatgaatttcaaattnacnagant 47
 ||||| | | | | | | | | | | | | | | | |
 Db 43 AATGAACCTAAAGACTTTTCACAGCAGATGAGT 12

RESULT 5
 AAI78837/C
 ID AAI78835 standard; DNA; 50 BP.
 AC AAI78835;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:5776.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 PD 07-JUN-2001.
 PF 30-NOV-2000; 2000WO-US32758.
 PR 30-NOV-1999; 99US-0168138.
 PR 29-NOV-2000; 2000US-0726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2001-356160/37.
 XX
 PT Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -

Claim 1; Page 2277; 2653pp; English.
 AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 sequences (I), which contain single nucleotide polymorphisms (SNPs).
 AA173060 to AA179867 represent peptides related to human polymorphic
 polynucleotide sequences. The sequences can be used in gene and protein
 therapy, and in vaccine production. (I) and the polypeptides encoded by
 them may be used in the prevention, diagnosis and treatment of diseases
 associated with inappropriate expression of polymorphic polypeptides.
 For example, (I) may be used to treat disorders by rectifying mutations
 or deletions in a patient's genome that affect the activity of
 polypeptides by expressing inactive proteins or to supplement the
 patients own production of polypeptide. Additionally, (I) and its
 complementary sequences may also be used as DNA probes in diagnostic
 assays to detect and quantitate the presence of similar nucleic acids
 in samples, and therefore which patients may be in need of restorative
 therapy. The polypeptides encoded by (I) may be used as antigens in the
 production of antibodies specific for polymorphic polypeptides. The
 antibodies may also be used to down regulate expression and activity.
 The antibodies may also be used as diagnostic agents for detecting the
 presence of polymorphic polypeptides in samples.
 Sequence 50 BP; 16 A; 7 C; 7 G; 20 T; 0 other;

Query Match 30.8%; Score 15.4; DB 22; Length 50;
 Best Local Similarity 59.4%; Pred. No. 3.1e+03;
 Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 16 aatgaatttcaaattnacnagant 47
 ||||| | | | | | | | | | | | | | | | |
 Db 40 AATGAACCTAAAGACTTTTCACAGCAGATGAGT 9

RESULT 6
 AAI78837/C
 ID AAI78837 standard; DNA; 50 BP.
 AC AAI78837;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:5778.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 PD 07-JUN-2001.
 PF 30-NOV-2000; 2000WO-US32758.
 PR 30-NOV-1999; 99US-0168138.
 PR 29-NOV-2000; 2000US-0726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2001-356160/37.
 XX
 PT Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy -

Claim 1; Page 2278; 2653pp; English.
 AA173060 to AA179867 represent isolated human polymorphic polynucleotide
 sequences (I), which contain single nucleotide polymorphisms (SNPs).
 AA173060 to AA179867 represent peptides related to human polymorphic
 polynucleotide sequences. The sequences can be used in gene and protein
 therapy, and in vaccine production. (I) and the polypeptides encoded by
 them may be used in the prevention, diagnosis and treatment of diseases
 associated with inappropriate expression of polymorphic polypeptides.
 For example, (I) may be used to treat disorders by rectifying mutations
 or deletions in a patient's genome that affect the activity of
 polypeptides by expressing inactive proteins or to supplement the
 patients own production of polypeptide. Additionally, (I) and its
 complementary sequences may also be used as DNA probes in diagnostic
 assays to detect and quantitate the presence of similar nucleic acids
 in samples, and therefore which patients may be in need of restorative
 therapy. The polypeptides encoded by (I) may be used as antigens in the
 production of antibodies specific for polymorphic polypeptides. The
 antibodies may also be used to down regulate expression and activity.
 The antibodies may also be used as diagnostic agents for detecting the
 presence of polymorphic polypeptides in samples.
 Sequence 50 BP; 16 A; 7 C; 8 G; 19 T; 0 other;

Query Match 30.8%; Score 15.4; DB 22; Length 50;
 Best Local Similarity 59.4%; Pred. No. 3.1e+03;
 Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 16 aatgaatttcaaattnacnagant 47
 ||||| | | | | | | | | | | | | | | | |
 Db 40 AATGAACCTAAAGACTTTTCACAGCAGATGAGT 9

```

RESULT 7
AAAT79137/C
ID AAAT79137 standard; DNA; 37 BP.
XX
XX AAAT79137;
AC
XX 08-OCT-1997 (first entry)
XX
XX Primer for luciferase luxAB reporter gene.
DE
XX
XX Primer: polymerase chain reaction; PCR; amplification; luxAB;
KW luciferase; reporter gene; Synechococcus; plasmid vector; ss.
XX
XX Synthetic.
OS
XX JP09140385-A.
PN
XX 03-JUN-1997.
PD
XX 20-NOV-1995; 95JP-0326586.
PF
XX 20-NOV-1995; 95JP-0326586.
PR
XX 20-NOV-1995; 95JP-0326586.
PA
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
XX
XX WPI; 1997-344898/32.
DR
XX
XX Thermally inducible Cyanobacterium Synechococcus vector - useful in
PT high degree, recombinant gene, expression systems
XX
XX Example 1; Page 4; 6pp; Japanese.
XX
XX The present sequence is a primer for the PCR amplification of the
CC luciferase luxAB reporter gene, which was used in the preparation
CC of a novel Synechococcus plasmid vector, comprising a partial
CC replication origin sequence in an intrinsic Synechococcus plasmid
CC and a lambda phage c1857 P1 promoter and repressor systems.
CC As the vector is thermally inducible, the multiplication of a
CC microorganism and the high level expression of a gene can be
CC carried out in different steps by controlling culture temperature.
CC The product of an arbitrary gene, whether intrinsic or extraneous,
CC can be produced in large amounts by Cyanobacterium Synechococcus.
CC Culture costs can be reduced as the Cyanobacterium can be cultured
CC in an inorganic medium, a pond or the ocean, making large scale
CC culture feasible as compared to E. coli and yeasts.
XX
XX Sequence 37 BP; 13 A; 7 C; 5 G; 12 T; 0 other;
SQ

```

Query Match 29.6%; Score 14.8; DB 18; Length 37;
 Best Local Similarity 72.7%; Pred. No. 5.3e+03;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

OY 14 anaatgaatttcaaatatna 35
    | | | | | | | | | | | | |
DB 33 AGAAGAACTTCCAAATTTCA 12

```

RESULT 8
 AAV60882
 ID AAV60882 standard; DNA; 39 BP.
 XX
 XX AAV60882;
 AC
 XX 25-JAN-1999 (first entry)
 XX
 XX Oligonucleotide 910373 for constructing MAB Vh region variants.
 DE
 XX
 XX Mutation: mutagenesis; antigen-binding region; monoclonal antibody;
 KW catalytic site; serine protease; complementarity determining region;
 KW walk-through, ss

```

XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX US5798208-A.
XX
XX 25-AUG-1998.
XX
XX 02-NOV-1992; 92US-0930600.
XX
XX 02-NOV-1992; 92US-0930600.
XX
XX 05-APR-1990; 90US-0505314.
XX
XX (CREM/) CREM R.
XX
XX Crea R;
XX
XX WPI; 1998-480376/41.
XX
XX Mutagenesis of pre-determined gene sequences - useful for systematic
PT changes of pre-determined amino acids to see their effect on protein
PT activity, and to create gene expression libraries
XX
XX Example 1; Column 21-22; 33pp; English.
XX
XX The invention relates to a method of generating mutations in proteins by
CC synthesizing a mixture of oligonucleotides in order to alter the codons
CC for specific amino acids within a defined region of the protein. Using
CC a range of oligonucleotides for the mutations, expression libraries of
CC the mutant protein can be constructed. As an example of the method, the
CC antigen-binding region of the monoclonal antibody (MAB) MCP603 (which
CC binds phosphocholine) is altered to contain the catalytic triad residues
CC for a serine protease. Specifically the amino acids to be altered are
CC selected from the Asp of the complementarity determining region (CDR) 1
CC region and the Ser of the CDR2 from the light chain variable region (VL).
CC CDR3 and the Ser of the CDR2 from the light chain variable region (VL).
CC The mutagenesis is by a "walk-through" method. Oligonucleotides
CC AAV60881-V60900 are used to assemble the Vh gene for monoclonal antibody
CC MCP603 for the construction of variants (see AAV60860-V60880).
XX
XX Sequence 39 BP; 11 A; 12 C; 4 G; 12 T; 0 other;
SQ

```

Query Match 29.2%; Score 14.6; DB 19; Length 39;
 Best Local Similarity 60.7%; Pred. No. 6.4e+03;
 Matches 17; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

OY 21 anttacaatttncgcnanagant 48
    | | | | | | | | | | | | |
DB 9 acttaccagtttaacttcagtgaatt 36

```

RESULT 9
 AAS17691/C
 ID AAS17691 standard; DNA; 41 BP.
 XX
 XX AAS17691;
 AC
 XX 19-FEB-2002 (first entry)
 XX
 XX Human GAPa protein 9 PCR oligonucleotide probe #1.
 DE
 XX
 XX Human; ss; GAPa protein 9; cancer; HIV; probe;
 KW human immunodeficiency virus infection.
 XX
 XX Homo sapiens.
 OS
 XX CN1313309-A.
 PN
 XX 19-SEP-2001.
 PD
 XX 10-MAR-2000; 2000CN-0111977.
 PF
 XX

Query Match 28.8%; Score 14.4; DB 20; Length 20;
 Best Local Similarity 83.3%; Pred. No. 7.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 16 aatgaantttacnaattt 33
 ||||| ||||| |||||
 DB 2 aatgaagttacaaact 19

RESULT 12

AA37753 standard; DNA; 20 BP.

AA37753;

09-JUL-1999 (first entry)

Staphylococcus sp. detecting oligonucleotide Fem2.

FemA; primer; identification; detection; therapy; infection; femB;

amplification; genotyping; gram-positive bacteria; vaccine; ss.

Synthetic

Staphylococcus sp.

W09916780-A2.

08-APR-1999.

28-SEP-1998; 98MO-BE00141.

26-SEP-1997; 97EP-0870146.

(BENA-) BELGIAN MIN NAT DEFENCE.

(UYLO-) UNIV CATHOLIQUE LOUVAIN.

Gala J, Yannuffel P;

WPI; 1999-287521/24.

New Staphylococcus-specific oligonucleotides

Claim 5; Page 8; 48pp; English.

This invention describes novel Staphylococcus-specific oligonucleotides

based on the consensus fema nucleotide sequence which are used to

develop products for the identification, detection and therapy of

infections. The oligonucleotides can be used for the genetic

amplification, the identification and/or quantification of various fema

sequences which are specific to known or unknown Staphylococci species.

Since the fema sequence is similar to the femB sequence, the

oligonucleotides can also be used for the molecular genotyping of fema

genes of different Staphylococci species or other gram-positive bacteria.

The fema nucleic acids can also be used in therapeutic applications.

They can also be used to identify inhibitors, e.g. antibodies or

antisense oligonucleotides, for blocking expression of the fema

nucleotide sequences. They can also be used for producing vaccines

against Staphylococci infections.

Sequence 20 BP; 8 A; 1 C; 2 G; 8 T; 1 other;

Query Match 28.8%; Score 14.4; DB 20; Length 20;

Best Local Similarity 88.9%; Pred. No. 7.2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 16 aatgaantttacnaattt 33

||||| ||||| |||||

DB 2 aatgaagttacnaact 19

RESULT 13

AA267280
 ID AA267280 standard; DNA; 47 BP.

AA267280;

10-SEP-2001 (first entry)

Human map-related biallelic marker SEQ ID NO:1627.

Human genome; biallelic marker; high density disequilibrium map;

genomic map; haplotype; phenotype; polymorphic base; genotyping;

haplotyping; hybridisation; identification; characterisation;

diagnosis; single nucleotide polymorphism; SNP; ds.

Homo sapiens.

Key

variation

28-OCT-1999.

21-APR-1999; 99MO-IB00822.

21-APR-1998; 98US-0082614.

23-NOV-1998; 98US-0109732.

(GSET) GENSET.

Cohen D, Blumenfeld M, Chumakov I;

WPI; 2000-013267/01.

Novel biallelic markers used to construct a high density disequilibrium

map of the human genome

Claim 1; Page 577; 2745pp; English.

AA265654 to AA269578 represent human biallelic markers from the present

invention, which contain a polymorphic base at position 24 of their

nucleotide sequences. AA269579 to AA277440 represent amplification

primers for the biallelic markers. The biallelic markers of the

invention have a variety of uses: they can be used for high density

mapping of the human genome, and in complex association studies and

haplotyping studies which are useful in determining the genetic basis

for disease states. Compositions and methods of the invention can also

be useful for the identification of the targets for the development of

pharmaceutical agents and diagnostic methods, as well as the

characterisation of the differential efficacious responses to and side

effects from pharmaceutical agents acting on a disease as well as other

treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297

and 3367, are not actually given a sequence in the Sequence Listing

from the present invention.

Sequence 47 BP; 17 A; 9 C; 10 G; 11 T; 0 other;

Query Match 28.8%; Score 14.4; DB 21; Length 47;

Best Local Similarity 58.1%; Pred. No. 7.8e+03;

Matches 18; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 14 anaatgaantttacnaattt 44

||||| ||||| |||||

DB 8 accatgaagttccacaaatgaatgtcagag 38

RESULT 14

AA267280

ID AA267280 standard; DNA; 33 BP.

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XX AAN80833;
AC
XX 30-NOV-1990 (first entry)
DT
XX
DE Probe no.2 for 16S rRNA of a broad phylogenetic range of bacteria.
XX
KW Bacteria; probe; 16S ribosomal RNA; ss.
XX
XX Synthetic.
OS
XX W08803957-A.
PN
XX
XX 02-JUN-1988.
PD
XX
XX 24-NOV-1987; 87WO-US03009.
PF
XX
XX 24-NOV-1986; 86US-0934244.
PR
XX 07-AUG-1987; 87US-0083542.
PR
XX (GENP-) GENPROBE INC.
PA
XX Hogan JJ, Smith RD, Kop JA, McDonough SH;
PI
XX WPI; 1988-161626/23.
DR
XX
XX Probes for non-viral organisms - comprising an oligonucleotide
PT complementary to a unique variable region rRNA sequence.
PT
XX
XX Claim 220; Page 161; 21lpp; English.
PS
XX
XX The probe is designed to hybridise with 16S rRNA in a broad range
CC of bacteria commonly found in urine, except Ureaplasma urealyticum
CC but not to yeast or human rRNA. It corresponds to bases 675-715
CC of the E. coli 16S rRNA and has a Tm of 69 deg.C.
CC See also AAN80785-N80851.
CC
XX
XX Sequence 33 BP; 7 A; 12 C; 6 G; 8 T; 0 other;
SQ

Query Match 28.4%; Score 14.2; DB 9; Length 33;
Best Local Similarity 64.0%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 19 gaantttacnaatttnacngcnana 43
||| ||| ||| ||| ||| |||
Db 4 gatctctacgcatttcacgcgtaca 28

RESULT 15
AAF23101
ID AAF23101 standard; DNA; 33 BP.
XX
XX AAF23101;
AC
XX
XX 20-MAR-2001 (first entry)
DT
XX
XX Bacterial rRNA specific sequence #2.
DE
XX
XX Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
KW Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
KW Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
KW bacterium; ss.
XX
XX Bacteria.
OS
XX
XX US6150517-A.
PN
XX
XX 21-NOV-2000.
PD
XX
XX 30-MAY-1995; 95US-0454063.
PF
XX
XX 22-FEB-1994; 94US-0200866.
PR
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PR 24-NOV-1987; 87US-0295208.
PR 24-NOV-1987; 87WO-US03009.
PR 11-DEC-1991; 91US-0806929.
PR 24-NOV-1986; 86US-0934244.
PR 07-AUG-1987; 87US-0083542.
XX
XX (GENP-) GEN-PROBE INC.
PA
XX McDonough SH, Kop JA, Smith RD, Hogan JJ;
XX
XX WPI; 2001-060029/07.
XX
XX Preparing a probe for nucleic acid hybridization assays comprises
PT constructing a nucleotide polymer sufficiently complementary to
PT hybridize to an rRNA region that distinguishes non-viral target from
PT non-viral non-target species -
XX
XX Example 19; Column 53; 75pp; English.
PS
XX
XX The present invention provides novel methods of producing probes for use
CC in the identification of a number of microorganisms. These include E.
CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
CC bacteria.
XX
XX Sequence 33 BP; 7 A; 12 C; 6 G; 8 T; 0 other;
SQ

Query Match 28.4%; Score 14.2; DB 22; Length 33;
Best Local Similarity 64.0%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 19 gaantttacnaatttnacngcnana 43
||| ||| ||| ||| ||| |||
Db 4 gatctctacgcatttcacgcgtaca 28

Search completed: June 20, 2002, 23:09:28
Job time: 30133 sec
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Fri Jun 21 08:38:16 2002

us-09-509-234c-1_copy_1_50.primer.rng

us-09-509-234c-1_copy_1_50.primer.rn1

OM nucleic - nucleic search, using SW model

Run on: June 20, 2002, 22:17:00 ; Search time 66.94 Seconds
(without alignments)
183.473 Million cell updates/sec

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Perfect score:	50
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 506208

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Minimum DB seq length: 15
Maximum DB seq length: 50

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post-processing: Minimum Match 0%
                  Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

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2	14.6	29.2	39	2	US-08-455-724A-5
3	14.6	29.2	47	1	US-08-122-433-7
4	13.8	27.6	45	4	US-09-315-793-4
5	13.6	27.2	32	2	US-08-452-724A-4
6	13.4	26.8	33	4	US-08-874-102-4
7	13.4	26.8	50	1	US-08-171-389-483
8	13.4	26.8	50	1	US-08-123-936-483
9	13.4	26.8	50	1	US-08-475-228A-483
10	13.4	26.8	50	3	US-08-482-080A-483
11	13.4	26.8	50	5	PCT-US93-12388-483
12	13.2	26.4	30	4	US-09-337-712-94
13	13.2	26.4	30	4	US-09-177-268-4
14	13.2	26.4	30	4	US-08-386-029A-62
15	13.2	26.4	50	3	US-08-675-566-58
16	13	26.0	22	3	US-08-224-657-62
17	13	26.0	22	3	US-08-675-566-58
18	13	26.0	22	4	US-09-354-138-82
19	13	26.0	22	4	US-08-480-481-5
20	13	26.0	30	1	US-08-368-395-5
21	13	26.0	35	1	US-08-162-836-6
22	12.8	25.6	48	1	US-09-397-168-66
23	12.8	25.6	22	1	US-08-273-776-5
24	12.8	25.6	22	2	US-08-598-607-1
25	12.8	25.6	31	1	US-08-276-852-39
26	12.8	25.6	31	1	US-08-133-011-15
27	12.8	25.6	31	1	US-08-387-874-83
28	12.8	25.6	31	1	US-08-899-595-39
29	12.4	24.8	72	2	US-08-459-951-6
30	12.4	24.8	72	2	US-08-600-656-13
31	12.4	24.8	73	3	US-09-354-191A-13
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35	12.4	24.8	78	12.4	
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52	12.4	24.0	30	1	US-08-629-001A-88
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54	12.4	24.0	30	3	US-08-642-274D-167
55	12.4	24.0	31	4	US-08-679-645-269
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57	12.4	24.0	33	1	US-08-480-525-17
58	12.4	24.0	33	3	US-08-674-984-4

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250	11.2	22.4	37	1	US-08-297-299B-56	Sequence 56, Appl
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252	11.2	22.4	37	2	US-08-858-083-12	Sequence 12, Appl
253	11.2	22.4	37	2	US-08-858-083-55	Sequence 55, Appl
254	11.2	22.4	37	2	US-08-858-083-56	Sequence 56, Appl
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282	11.2	22.4	44	4	US-08-242-038-37	Sequence 20, Appl
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288	11.2	22.4	47	4	US-09-338-907-191	Sequence 191, App
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299	11.2	22.4	21	1	US-08-158-232-27	Sequence 27, Appl
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307	11.2	22.4	21	5	PCT-US94-07902-11	Sequence 3, Appl
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313	11.2	22.4	27	3	US-08-195-006-11	Sequence 11, Appl
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315	11.2	22.4	27	5	PCT-US94-07644A-11	Sequence 7, Appl
316	11.2	22.4	28	1	US-08-387-315A-7	Sequence 7, Appl
317	11.2	22.4	28	2	US-08-754-535-7	Sequence 16, Appl
318	11.2	22.4	28	2	US-08-756-506-16	Sequence 924, App
319	11.2	22.4	28	2	US-08-859-998-924	Sequence 924, App

us-09-509-234c-1_copy_1_50.primer.rni

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Sequence 59, Appl
Sequence 171, Appl
Sequence 326, App
Sequence 136, App
Sequence 141, App
Sequence 12, Appl
Sequence 117, App
Sequence 136, App
Sequence 141, App
Sequence 78, Appl
Sequence 111, App
Sequence 111, App
Sequence 44, Appl
Sequence 6, Appl
Sequence 19, Appl
Sequence 111, App
Sequence 6, Appl
Sequence 82, Appl
Sequence 82, Appl

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; Best Local Similarity 77.3%; Pred. No. 1.5e+02;
; Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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DB 17 AAATGAAGTTAACTAATTCA 38
RESULT 2
US-08-452-724A-5
; Sequence 5, Application US/08452724A
; Patent No. 5830650
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: Walk-Through Mutagenesis
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,724A
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,600
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02362
; FILING DATE: 05-APR-1991
; APPLICATION NUMBER: US 07/505,314
; FILING DATE: 05-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq. David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: RC90-01AZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-452-724A-5
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Best Local Similarity 60.7%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 21 antttacnaattttacnagcnanagantt 48
DB 9 ACTCTACCAGTTTAACTTCATGGAATT 36
RESULT 3
US-08-122-433-7/c

Sequence 59, Appl
Sequence 171, Appl
Sequence 326, App
Sequence 136, App
Sequence 141, App
Sequence 12, Appl
Sequence 117, App
Sequence 136, App
Sequence 141, App
Sequence 78, Appl
Sequence 111, App
Sequence 111, App
Sequence 44, Appl
Sequence 6, Appl
Sequence 19, Appl
Sequence 111, App
Sequence 6, Appl
Sequence 82, Appl
Sequence 82, Appl

US-08-923-536A-10
; Sequence 10, Application US/08923536A
; Patent No. 5965426
; GENERAL INFORMATION:
; APPLICANT: SAKAI, Yasuyoshi
; APPLICANT: KATO, No. 5965426uo
; APPLICANT: SHIBANO, Yui
; TITLE OF INVENTION: PROTEIN DISULFIDE ISOMERASE GENE DERIVED
; FROM STRAIN OF METHYLOTROPIC YEAST
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,536A
; FILING DATE: 04-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-234287
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 001560-317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid

Sequence 7, Application US/08122433
Patent No. 5683985
GENERAL INFORMATION:
APPLICANT: Chu, Barbara C.F.
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND
TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH
TITLE OF INVENTION: SELECTIVELY BIND TO DEFINED DNA SEQUENCES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,433
FILING DATE: 22-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,337
FILING DATE: 18-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 9308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-122-433-7

Query Match 29.2%; Score 14.6; DB 1; Length 47;
Best Local Similarity 60.7%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 20 aatttcaaattnacngcnagant 47
DB 47 AATTTCATATACATATAGAGAA 20

RESULT 4
US-09-315-793-4/C
Sequence 4, Application US/09315793
Patent No. 6221597
GENERAL INFORMATION:
APPLICANT: Roberts, Christopher J.
TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-048
CURRENT APPLICATION NUMBER: US/09/315,793
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-315-793-4

Query Match 27.6%; Score 13.8; DB 4; Length 45;
Best Local Similarity 56.2%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 17 atgaanttcaaattnacngcnagant 48
DB 34 ATGATTTTCTTTATTAACCGAATATAGAT 3

RESULT 5
US-08-452-724A-4/C
Sequence 4, Application US/08452724A
Patent No. 5830650
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: Walk-Through Mutagenesis
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,724A
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,600
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02362
FILING DATE: 05-APR-1991
APPLICATION DATA: PCT/US91/02362
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA: US 07/505,314
APPLICATION NUMBER: US 07/505,314
FILING DATE: 05-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: RC90-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-452-724A-4

Query Match 27.2%; Score 13.6; DB 2; Length 30;
Best Local Similarity 61.5%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 23 ttacnaatttnacngcnagant 48
DB 29 TCTACAGTTTACTTCATGGAAT 4

RESULT 6
US-08-874-102-24

us-09-509-234c-1_copy_1_50.primer.rni

Fri Jun 21 08:38:16 2002

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; Sequence 24, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,102
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-2-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; US-08-874-102-24

Query Match 26.88; Score 13.4; DB 4; Length 33;
Best Local Similarity 77.88; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 14 anaatgaatttacnaat 31
Db 10 AGAATGAATTTACAGAT 27

RESULT 7
US-08-171-389-483/c
; Sequence 483, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:

; Sequence 24, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,102
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-2-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; US-08-874-102-24

Query Match 26.88; Score 13.4; DB 1; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 19 gaatttcacnaatttcacnaaganttt 48
Db 30 GCATTTTTATTATTATTCAGCAGGTGAGGT 1

RESULT 8
US-08-123-936-483/c
; Sequence 483, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 483:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Bovine leukemia virus
US-08-123-936-483

Query Match      26.8%; Score 13.4; DB 1; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 19 gaattacnaattacgacgagtgaggt 48
Db 30 GCATTATTATATTATTCACGACGTGAGGT 1

RESULT 9
US-08-475-228A-483/C
Sequence 483, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
```

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 483:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Bovine leukemia virus
US-08-475-228A-483

Query Match      26.8%; Score 13.4; DB 2; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 19 gaattacnaattacgacgagtgaggt 48
Db 30 GCATTATTATATTATTCACGACGTGAGGT 1

RESULT 10
US-08-482-080A-483/C
Sequence 483, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
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; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 483:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Bovine leukemia virus
; US-08-482-080A-483

Query Match 26.8%; Score 13.4; DB 3; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 19 gaatttacaatttgcacgaggtgaggt 48
| | | | | | | | | | | | | | | | | | | | | |
Db 30 GCATTTTATTATTTATCAGCAGGTGAGGT 1

RESULT 11
PCT-US93-12388-483/c
; Sequence 483, Application PC/TUS9312388
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12388
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 483:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Bovine leukemia virus
; PCT-US93-12388-483

Query Match 26.8%; Score 13.4; DB 5; Length 50;
Best Local Similarity 56.7%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 19 gaatttacaatttgcacgaggtgaggt 48
| | | | | | | | | | | | | | | | | | | | | |
Db 30 GCATTTTATTATTTATCAGCAGGTGAGGT 1

RESULT 12
US-09-237-712-94
; Sequence 94, Application US/09237712
; Patent No. 6180391
; GENERAL INFORMATION:
; APPLICANT: BROWN, WILLIAM C.
; TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS
; TITLE OF INVENTION: GENES IN E. COLI
; FILE REFERENCE: A-518
; CURRENT APPLICATION NUMBER: US/09/237,712
; CURRENT FILING DATE: 1999-01-26
; EARLIER APPLICATION NUMBER: 60/072,794
; EARLIER FILING DATE: 1998-01-28
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 94
; LENGTH: 30
; TYPE: DNA
; ORGANISM: oligonucleotide
; US-09-237-712-94

Query Match 26.4%; Score 13.2; DB 4; Length 30;
Best Local Similarity 62.5%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 24 ttacnaatttgcacgaggtgaggt 47
| | | | | | | | | | | | | | | | | | | | | |
Db 2 ttacgaatttgcacgaggtgaggt 25

RESULT 13
US-09-177-268-4/c
; Sequence 4, Application US/09177268
; Patent No. 6203986
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Bertrand, Edoard
; TITLE OF INVENTION: VISUALIZATION OF RNA IN LIVING CELLS
; FILE REFERENCE: 10445/002001
; CURRENT APPLICATION NUMBER: US/09/177,268
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: most probably a yeast
; US-09-177-268-4

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Query Match 26.4%; Score 13.2; DB 4; Length 30;
Best Local Similarity 68.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 17 atgaattacnaattcnaag 38
||||| ||||| ||||| |||||
DB 26 ATGAATTGTAACAAGTCGACAG 5

RESULT 14
US-08-388-029A-62/c
Sequence 62, Application US/08388029A
Patent No. 6110665

GENERAL INFORMATION:

APPLICANT: FENGER, CLARA K.
APPLICANT: GRANSTROM, DAVID R.
APPLICANT: GAJDAR, ALVIN A.
TITLE OF INVENTION: SARCOCYTIS NEURONA DIAGNOSTIC PRIMER
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOME, PRICE, LEBLANC & BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: US
ZIP: 22114

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,029A
FILING DATE: 14-FEB-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PRICE, ROBERT L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 434-046
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-388-029A-62

Query Match 26.4%; Score 13.2; DB 3; Length 50;
Best Local Similarity 64.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 20 aaattacnaattcnaagcnaag 44
||||| ||||| ||||| |||||
DB 31 AAATCTAGAAATTCTACACTCTNNAG 7

RESULT 15

US-08-224-657-82/c
Sequence 82, Application US/08224657
Patent No. 5756102
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Taylor, Jill
TITLE OF INVENTION: POXYVIRUS - CANINE DISTEMPER VIRUS (CDV)

TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
TITLE OF INVENTION: RECOMBINANTS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,657
FILING DATE: 06-APR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-224-657-82

Query Match 26.0%; Score 13; DB 1; Length 22;
Best Local Similarity 86.7%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 tgaatttactaatt 32
||||| ||||| |||||
DB 17 TGAATTTACTAATT 3

Search completed: June 20, 2002, 23:43:09
Job time: 5169 sec

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Fri Jun 21 08:38:18 2002

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967 9.4 18.8 34 12 AZ773199
968 9.4 18.8 34 12 AZ804613
969 9.4 18.8 35 9 AW246486
970 9.4 18.8 35 10 C00974
971 9.4 18.8 35 10 C02011
972 9.4 18.8 35 10 D25857
973 9.4 18.8 35 12 AZ339968
974 9.4 18.8 35 12 AZ988042
975 9.4 18.8 36 9 AI448911
976 9.4 18.8 36 9 AJ239830
977 9.4 18.8 36 10 B077368
978 9.4 18.8 36 10 BE873179
979 9.4 18.8 36 12 AZ345952
980 9.4 18.8 36 12 AZ465655
981 9.4 18.8 36 12 AZ601632
982 9.4 18.8 36 12 AZ626864
983 9.4 18.8 36 12 TAI64B05Q
984 9.4 18.8 37 9 AA948700
985 9.4 18.8 37 9 AV852744
986 9.4 18.8 37 10 C21198
987 9.4 18.8 37 12 AZ503091
988 9.4 18.8 38 10 D19137
989 9.4 18.8 38 10 D19987
990 9.4 18.8 38 12 AZ662729
991 9.4 18.8 39 9 AU010358
992 9.4 18.8 39 9 AU010360
993 9.4 18.8 39 9 AU011886
994 9.4 18.8 39 10 BJ047458
995 9.4 18.8 39 10 BE512831
996 9.4 18.8 39 12 AZ308441
997 9.4 18.8 39 12 AZ321053
998 9.4 18.8 39 12 AZ491341
999 9.4 18.8 39 12 AZ595854
c1000 9.4 18.8 39 12 AZ596555

ALIGNMENTS

AZ368099 46 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0118602F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0118602 F, DNA sequence.
ACCESSION AZ368099
VERSION 1 GI:10481799
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0118 row: G column: 02
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers

```

```

RESULT 1
AZ368099/c 46 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0466A22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0466A22 R, DNA sequence.
ACCESSION AZ368099
VERSION 1 GI:11748729
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0466 row: A column: 22
Seq primer: CACACAGGAACGACGTATGACC
Class: plasmid ends
High quality sequence stop: 40.

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BASE COUNT 12 a 5 c 14 g 15 t
ORIGIN
17 atgaattatcnaatttncgncnagantt 48
37 ATGAATTTGCCACCATCCTCCAAAACCTT 6

Query Match 30.8% Score 15.4; DB 12; Length 46;
Best Local Similarity 59.4%; Pred. No. 4.1e-04;
Matches 19; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 atgaattatcnaatttncgncnagantt 48
DB 37 ATGAATTTGCCACCATCCTCCAAAACCTT 6

RESULT 2
AZ368539/c 40 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0466A22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0466A22 R, DNA sequence.
ACCESSION AZ368539
VERSION 1 GI:11748729
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0466 row: A column: 22
Seq primer: CACACAGGAACGACGTATGACC
Class: plasmid ends
High quality sequence stop: 40.

```

Location/Qualifiers

14 a	4 c	5 g	17 e
------	-----	-----	------

9 a	10 c	7 g
-----	------	-----

28.88; Score 14.4; DB 9; Length 40;

0; Mismatches 13; Indels 0; Gaps 0;

aattnacngcnag 44

ACTTTCACAGGTAGAG 1

44 bp

CI_CGAP_Lu29 Mus m

IT:9313062

tazoa: Chordata; C

heria; Rodentia; S

44) 44b 44c 44d 44e 44f 44g 44h 44i 44j 44k 44l 44m 44n 44o 44p 44q 44r 44s 44t 44u 44v 44w 44x 44y 44z 44aa 44ab 44ac 44ad 44ae 44af 44ag 44ah 44ai 44aj 44ak 44al 44am 44an 44ao 44ap 44aq 44ar 44as 44at 44au 44av 44aw 44ax 44ay 44az 44ba 44bb 44bc 44bd 44be 44bf 44bg 44bh 44bi 44bj 44bk 44bl 44bm 44bn 44bo 44bp 44bq 44br 44bs 44bt 44bu 44bv 44bw 44bx 44by 44bz 44ca 44cb 44cc 44cd 44ce 44cf 44cg 44ch 44ci 44cj 44ck 44cl 44cm 44cn 44co 44cp 44cq 44cr 44cs 44ct 44cu 44cv 44cw 44cx 44cy 44cz 44da 44db 44dc 44dd 44de 44df 44dg 44dh 44di 44dj 44dk 44dl 44dm 44dn 44do 44dp 44dq 44dr 44ds 44dt 44du 44dv 44dw 44dx 44dy 44dz 44ea 44eb 44ec 44ed 44ee 44ef 44eg 44eh 44ei 44ej 44ek 44el 44em 44en 44eo 44ep 44eq 44er 44es 44et 44eu 44ev 44ew 44ex 44ey 44ez 44fa 44fb 44fc 44fd 44fe 44ff 44fg 44fh 44fi 44fj 44fk 44fl 44fm 44fn 44fo 44fp 44fq 44fr 44fs 44ft 44fu 44fv 44fw 44fx 44fy 44fz 44ga 44gb 44gc 44gd 44ge 44gf 44gg 44gh 44gi 44gj 44gk 44gl 44gm 44gn 44go 44gp 44gq 44gr 44gs 44gt 44gu 44gv 44gw 44gx 44gy 44gz 44ha 44hb 44hc 44hd 44he 44hf 44hg 44hh 44hi 44hj 44hk 44hl 44hm 44hn 44ho 44hp 44hq 44hr 44hs 44ht 44hu 44hv 44hw 44hx 44hy 44hz 44ia 44ib 44ic 44id 44ie 44if 44ig 44ih 44ii 44ij 44ik 44il 44im 44in 44io 44ip 44iq 44ir 44is 44it 44iu 44iv 44iw 44ix 44iy 44iz 44ja 44jb 44jc 44jd 44je 44jf 44jg 44jh 44ji 44jj 44jk 44jl 44jm 44jn 44jo 44jp 44jq 44jr 44js 44jt 44ju 44jv 44jw 44jx 44jy 44jz 44ka 44kb 44kc 44kd 44ke 44kf 44kg 44kh 44ki 44kj 44kk 44kl 44km 44kn 44ko 44kp 44kq 44kr 44ks 44kt 44ku 44kv 44kw 44kx 44ky 44kz 44la 44lb 44lc 44ld 44le 44lf 44lg 44lh 44li 44lj 44lk 44ll 44lm 44ln 44lo 44lp 44lq 44lr 44ls 44lt 44lu 44lv 44lw 44lx 44ly 44lz 44ma 44mb 44mc 44md 44me 44mf 44mg 44mh 44mi 44mj 44mk 44ml 44mm 44mn 44mo 44mp 44mq 44mr 44ms 44mt 44mu 44mv 44mw 44mx 44my 44mz 44na 44nb 44nc 44nd 44ne 44nf 44ng 44nh 44ni 44nj 44nk 44nl 44nm 44nn 44no 44np 44nq 44nr 44ns 44nt 44nu 44nv 44nw 44nx 44ny 44nz 44oa 44ob 44oc 44od 44oe 44of 44og 44oh 44oi 44oj 44ok 44ol 44om 44on 44oo 44op 44oq 44or 44os 44ot 44ou 44ov 44ow 44ox 44oy 44oz 44pa 44pb 44pc 44pd 44pe 44pf 44pg 44ph 44pi 44pj 44pk 44pl 44pm 44pn 44po 44pp 44pq 44pr 44ps 44pt 44pu 44pv 44pw 44px 44py 44pz 44qa 44qb 44qc 44qd 44qe 44qf 44qg 44qh 44qi 44qj 44qk 44ql 44qm 44qn 44qo 44qp 44qq 44qr 44qs 44qt 44qu 44qv 44qw 44qx 44qy 44qz 44ra 44rb 44rc 44rd 44re 44rf 44rg 44rh 44ri 44rj 44rk 44rl 44rm 44rn 44ro 44rp 44rq 44rr 44rs 44rt 44ru 44rv 44rw 44rx 44ry 44rz 44sa 44sb 44sc 44sd 44se 44sf 44sg 44sh 44si 44sj 44sk 44sl 44sm 44sn 44so 44sp 44sq 44sr 44ss 44st 44su 44sv 44sw 44sx 44sy 44sz 44ta 44tb 44tc 44td 44te 44tf 44tg 44th 44ti 44tj 44tk 44tl 44tm 44tn 44to 44tp 44tq 44tr 44ts 44tt 44tu 44tv 44tw 44tx 44ty 44tz 44ua 44ub 44uc 44ud 44ue 44uf 44ug 44uh 44ui 44uj 44uk 44ul 44um 44un 44uo 44up 44uq 44ur 44us 44ut 44uu 44uv 44uw 44ux 44uy 44uz 44va 44vb 44vc 44vd 44ve 44vf 44vg 44vh 44vi 44vj 44vk 44vl 44vm 44vn 44vo 44vp 44vq 44vr 44vs 44vt 44vu 44vv 44vw 44vx 44vy 44vz 44wa 44wb 44wc 44wd 44we 44wf 44wg 44wh 44wi 44wj 44wk 44wl 44wm 44wn 44wo 44wp 44wq 44wr 44ws 44wt 44wu 44wv 44ww 44wx 44wy 44wz 44xa 44xb 44xc 44xd 44xe 44xf 44xg 44xh 44xi 44xj 44xk 44xl 44xm 44xn 44xo 44xp 44xq 44xr 44xs 44xt 44xu 44xv 44xw 44xx 44xy 44xz 44ya 44yb 44yc 44yd 44ye 44yf 44yg 44yh 44yi 44yj 44yk 44yl 44ym 44yn 44yo 44yp 44yq 44yr 44ys 44yt 44yu 44yv 44yw 44yx 44yy 44yz 44za 44zb 44zc 44zd 44ze 44zf 44zg 44zh 44zi 44zj 44zk 44zl 44zm 44zn 44zo 44zp 44zq 44zr 44zs 44zt 44zu 44zv 44zw 44zx 44zy 44zz

<http://myc.nca.nih.gov/>

(1999)

ert Strausberg, Ph.D.

ement: Gilbert Sml
3 - T cella.l: nlin.gov

Preparation: Life

Arrayed by: The I

Cloning by: MGC clone

the I.M.A.G.E. Co

11n1.gov

sequence stop: 44.

Qualifiers

44

musculus

Xref="taxon:10090"

one="IMAGE:3586538"

one_lib="NCI_CGAP_L

issue_type: "cell origin"

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b_host="DH10B"
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te-"Organ: Lung; Ve

ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

REFERENCE 1 (bases 1 to 42)
AUTHORS Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B. N., Pl. M., Sato, T., Takemoto, K., Yasukawa, H., Williams, U., Maeda, M., Takeuchi, I., Ochial, H. and Tanaka, Y.

TITLE Developmental cDNA in Dictyostelium discoideum
JOURNAL Unpublished (1998)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan.

FEATURES
source
1: 42
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLD765"
/clone_1lb="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="sing"

BASE COUNT 23 a 1 c 3 g 15 t
ORIGIN

Query Match 27.6%; Score 13.8; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 16 aatgaattacnaattta 35
DB 37 AATTGATTTTACAAATTAA 18

RESULT 8
A2332059 46 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0060A16F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0060A16 F, DNA sequence.
ACCESSION A2332059
VERSION A2332059.1 GI:10395348
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 46)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: A column: 16
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
1: 46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UGCM0060A16"
/clone_1lb="Mouse 10kb plasmid UGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (q1473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 8 c 4 g 21 t
ORIGIN

Query Match 27.6%; Score 13.8; DB 12; Length 46;
Best Local Similarity 71.4%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 19 gaattacnaatttncgnc 39
DB 2 GACATTTATTAATTACAGC 22

RESULT 9
A2445660 50 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0241007R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0241007 R, DNA sequence.
ACCESSION A2445660
VERSION A2445660.1 GI:10595702
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0241 row: O column: 07
Seq primer: CACACAGGAACACGTATGAC
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
1: 50
/organism="Mus musculus"
/strain="C57BL/6J"


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/db_xref="taxon:10090"
/clone="UGGCM041007"
/clone_lib="Mouse 10kb plasmid UGGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPD42 (gi:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      15 a   11 c   8 g   16 t
ORIGIN
Query Match.          27.6%; Score 13.8; DB 12; Length 50;
Best Local Similarity 56.2%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 16 aatgaatttcaaattnacnncanagant 47
      ||||| ||| | | | | | | | | | |
Db 38 AATGATTTCCTTCAATTTAGCGGTAGAAT 7

RESULT 10
AA921415
LOCUS       AA921415
DEFINITION vzw37e06.r1 Soares_thymus_2NDMT Mus musculus CDNA clone
IMAGE:1328674 5' similar to TR:004892 004892 CYTOCHROME P450
LIKE_TBP,, mRNA sequence.
AA921415
AA921415.1 GI:3068194
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:688218
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone_lib="IMAGE:1328674"
    /clone="Soares_thymus_2NDMT"
    /sex="male"
    /issue_type="Thymus"
    /dev_stage="4 weeks"
    /lab_host="PH10B"
    /note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTAGTGAGCGCCGCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      11 a   11 c   10 g   14 t
ORIGIN
Query Match          26.8%; Score 13.4; DB 9; Length 46;
Best Local Similarity 58.6%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 16 aatgaatttcaaattnacnncanag 44
      ||||| ||| | | | | | | | | | |
Db 8 AATGAATTTCCTTCACTTGCATTCAGAG 36

RESULT 11
AA9218672/c
LOCUS       AA9218672
DEFINITION clome UGGC1M0450G08 R, DNA sequence.
ACCESSION  AA9218672
VERSION     AA9218672.1 GI:11740958
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0450 row: G column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UGGCM0450G08"
    /clone_lib="Mouse 10kb plasmid UGGC1M library"

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/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="108d05"

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ACCESSION	AZ402049
VERSION	AZ402649.1
KEYWORDS	GSS.
SOURCE	mus mouse.
ORGANISM	Mus musculus

Fri Jun 21 08:38:18 2002

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: N column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
FEATURES
source
1..45
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0269N11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 15 a 5 c 2 g 23 t
ORIGIN
Query Match 26.4%; Score 13.2; DB 12; Length 45;
Best Local Similarity 68.2%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 14 anaatgaattacnaatttna 35
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DB 24 AAAATTAAATTTATGAATTTGA 3
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RESULT 15
AZ798012/c 48 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0054002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0054002 R, DNA sequence.
ACCESSION AZ798012
VERSION AZ798012.1 GI:12947682
KEYWORDS GSS.
SOURCE house mouse.

REFERENCE 1 (bases 1 to 48)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: O column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
Location/Qualifiers
FEATURES
source
1..48
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0054O02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 12 a 4 c 11 g 21 t
ORIGIN
Query Match 26.4%; Score 13.2; DB 12; Length 48;
Best Local Similarity 68.2%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 14 anaatgaattacnaatttna 35
|||||
DB 28 AAAATTATCATGTACAAATTTAA 7
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Search completed: June 20, 2002, 23:05:02
Job time: 31067 sec

Fri Jun 21 08:38:18 2002

us-09-509-234c-1_copy_1_50.primer.rst

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:42:07 ; Search time 1932.32 Seconds
(Without alignments)
498.168 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1000_1045
Perfect score: 46
Sequence: 1 ngcngtggacnctcaatn.....gncantlcnngnagntat 46

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 663590

Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenBankl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
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15: em_ba:*
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28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query	Score	Match	Length	DB	ID	Description
SUMMARIES							

1	14	30.4	38	6	AX218691	AX218691 Sequence
2	13.6	29.6	50	6	AR148155	AR148155 Sequence
3	13.2	28.7	49	6	AR050507	AR050507 Sequence
4	13.2	28.7	49	6	AR124635	AR124635 Sequence
5	13.2	28.7	49	6	AX279805	AX279805 Sequence
6	13	28.3	33	6	AR003749	AR003749 Sequence
7	13	28.3	33	6	AR010085	AR010085 Sequence
8	13	28.3	33	6	AR055291	AR055291 Sequence
9	13	28.3	33	6	AR141220	AR141220 Sequence
10	13	28.3	33	6	AR141457	AR141457 Sequence
11	13	28.3	50	1	HEA37ND2	HEA37ND2
12	12.8	27.8	45	6	E60005	E60005
13	12.8	27.8	47	6	AX234992	AX234992 Sequence
14	12.8	27.8	48	6	I07868	I07868 Sequence
15	12.6	27.4	35	6	I05266	I05266 Sequence
16	12.6	27.4	45	6	AR033949	AR033949 Sequence
17	12.6	27.4	45	6	AR175082	AR175082 Sequence
18	12.6	27.4	45	6	AX032526	AX032526 Sequence
19	12.6	27.4	48	6	I07867	I07867 Sequence
20	12.4	27.0	47	6	AX194744	AX194744 Sequence
21	12.4	27.0	50	6	AR087173	AR087173 Sequence
22	12.4	27.0	50	6	E36072	E36072
23	12.4	27.0	50	6	I49628	I49628 Sequence
24	12.2	26.5	49	6	AR158009	AR158009 Sequence
25	12.2	26.5	49	6	AX279837	AX279837 Sequence
26	12.2	26.5	50	6	A06298	A06298
27	12.2	26.5	50	6	A10987	A10987
28	12.2	26.5	50	6	A11836	A11836
29	12	26.1	38	6	AX219011	AX219011 Sequence
30	12	26.1	38	6	AX219542	AX219542 Sequence
31	12	26.1	38	6	AX219543	AX219543 Sequence
32	12	26.1	38	6	AX219574	AX219574 Sequence
33	12	26.1	38	6	AX227864	AX227864 Sequence
34	12	26.1	41	6	I09032	I09032 Sequence
35	12	26.1	45	6	AX021022	AX021022 Sequence
36	12	26.1	45	6	AX081634	AX081634 Sequence
37	12	26.1	45	6	AX343665	AX343665 Sequence
38	12	26.1	48	6	AR065588	AR065588 Sequence
39	12	26.1	48	6	AR105964	AR105964 Sequence
40	12	26.1	50	6	AX164966	AX164966 Sequence
41	12	26.1	50	6	I42278	I42278 Sequence
42	11.8	25.7	28	6	AR090955	AR090955 Sequence
43	11.8	25.7	36	6	AX010623	AX010623 Sequence
44	11.8	25.7	37	6	AR153417	AR153417 Sequence
45	11.8	25.7	42	6	I22762	I22762 Sequence
46	11.8	25.7	42	6	I47587	I47587 Sequence
47	11.8	25.7	43	10	AB03552510	AB03552510
48	11.8	25.7	46	6	A98794	A98794
49	11.8	25.7	46	6	AR087647	AR087647 Sequence
50	11.8	25.7	47	6	AR170381	AR170381 Sequence
51	11.8	25.7	48	9	HUMDE06M3	HUMDE06M3
52	11.8	25.7	49	6	AR003532	AR003532 Sequence
53	11.8	25.7	49	6	AR087646	AR087646 Sequence
54	11.8	25.7	49	6	AX279743	AX279743 Sequence
55	11.8	25.7	49	6	AX305185	AX305185 Sequence
56	11.8	25.7	49	6	I55645	I55645 Sequence
57	11.6	25.2	26	6	AR156510	AR156510 Sequence
58	11.6	25.2	31	6	AR142157	AR142157 Sequence
59	11.6	25.2	31	6	BD007211	BD007211 Method an
60	11.6	25.2	34	6	AR031382	AR031382 Sequence
61	11.6	25.2	34	6	BD008750	BD008750 Composi11
62	11.6	25.2	36	6	AR130208	AR130208 Sequence
63	11.6	25.2	36	6	AR174240	AR174240 Sequence
64	11.6	25.2	38	6	AX219059	AX219059 Sequence
65	11.6	25.2	39	6	BD011043	BD011043 HIV probe
66	11.6	25.2	40	6	A63304	A63304 Sequence 2
67	11.6	25.2	40	6	A60185	A60185 Sequence 2
68	11.6	25.2	45	6	AR040813	AR040813 Sequence
69	11.6	25.2	26	6	AR167267	AR167267 Sequence
70	11.4	24.8	30	6	I33767	I33767 Sequence 29
71	11.4	24.8	34	6	A67363	A67363 Sequence 11
72	11.4	24.8	34	6	AR009703	AR009703 Sequence
73	11.4	24.8	34	6	AX137684	AX137684 Sequence

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Fri Jun 21 14:51:59 2002

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source          1. .33
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BASE COUNT      9 a 11 c 6 g 7 t
ORIGIN

Query Match     28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnntnnnncantngc 36
    ||||| | | | | | | | |
Db 23 TCAATGACTGTGGCAGTGGC 1

RESULT 9
LOCUS      ARI141220          33 bp      DNA
DEFINITION Sequence 39 from patent US 6146631.
ACCESSION  ARI141220
VERSION     ARI141220.1 GI:15100737
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE       Immunotoxins comprising ribosome-inactivating proteins
JOURNAL     Patent: US 6146631-A 39 14-NOV-2000;
FEATURES    Location/Qualifiers
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BASE COUNT  9 a 11 c 6 g 7 t
ORIGIN

Query Match     28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnntnnnncantngc 36
    ||||| | | | | | | | |
Db 23 TCAATGACTGTGGCAGTGGC 1

RESULT 10
LOCUS      ARI141457/c       33 bp      DNA
DEFINITION Sequence 39 from patent US 6146850.
ACCESSION  ARI141457
VERSION     ARI141457.1 GI:15100973
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Better,M.D. and Carroll,S.F.
TITLE       Proteins encoding gelonin sequences
JOURNAL     Patent: US 6146850-A 39 14-NOV-2000;
FEATURES    Location/Qualifiers
             source          1. .33
             /organism="unknown"
BASE COUNT  9 a 11 c 6 g 7 t
ORIGIN

Query Match     28.3%; Score 13; DB 6; Length 33;
Best Local Similarity 56.5%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnntnnnncantngc 36
    ||||| | | | | | | | |
Db 23 TCAATGACTGTGGCAGTGGC 1

RESULT 11
LOCUS      HEA37NU2/c       50 bp      DNA
DEFINITION H.influenzae non-uptake non-binding sequence 37nu2.
ACCESSION  M33438
VERSION     M33438.1 GI:148840
KEYWORDS
SOURCE      H.influenzae (strain Rd) DNA.
ORGANISM    Haemophilus influenzae
             Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
             Haemophilus.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Goodgal,S.H. and Mitchell,M.A.
JOURNAL     Unpublished (1990)
REFERENCE   2 (sites)
AUTHORS     Goodgal,S.H. and Mitchell,M.A.
TITLE       Sequence and uptake specificity of cloned sonicated fragments of
             Haemophilus influenzae DNA
JOURNAL     J. Bacteriol. 172, 5924-5928 (1990)
MEDLINE     91008969
COMMENT     [2] sites. [1] for [2].
             Draft entry and computer-readable sequence for [2],[1] kindly
             submitted by S.H.Goodgal, 30-MAR-1990.
             Author Address: S.H. Goodgal, and M.A. Mitchell, Dept. of
             Microbiology, School of Medicine, Rm 346, Johnson Pav.,
             Philadelphia, PA 19104-6076.
FEATURES    Location/Qualifiers
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BASE COUNT  15 a 13 c 15 g 7 t
ORIGIN

Query Match     28.3%; Score 13; DB 1; Length 50;
Best Local Similarity 47.1%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 3 cnggtggaactcnaatnnntnnnncantngc 36
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Db 34 CCGCTGGGACTTCATCCTCANTAGTGGCTTACGC 1

RESULT 12
LOCUS      E60005          45 bp      DNA
DEFINITION Ceramide-binding peptide.
ACCESSION  E60005
VERSION     E60005.1 GI:18622764
KEYWORDS    JP 2000319296-A/5.
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 45)
AUTHORS     Ishikawa,M., Tanaka,Y., Ogino,K. and Taki,T.
TITLE       Ceramide-binding peptide
JOURNAL     Patent: JP 2000319296-A 5 21-NOV-2000;
             OTSUKA PHARMACEUT CO LTD
COMMENT     OS Artificial Sequence
             PN JP 2000319296-A/5
             PD 21-NOV-2000
             PF 10-MAY-1999 JP 1999128674
             PR MASARU ISHIKAWA,YOSHINORI TANAKA,KOICHI OGINO,TAKAO TAKI PC
             C07K7/00
             CC Key
             FH Location/Qualifiers
             FT source
             FT /organism="Artificial Sequence".

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Query Match          27.8%; Score 12.8; DB 6; Length 48;
Best Local Similarity 43.8%; Pred. No. 1.9e+05;
Matches 14; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY      8  ggnactcnaatnntnnngcanticngcng 39
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Db      10  GGACTCATGNNGCATCTCCGACGCTTGACAG 41

RESULT 15
LOCUS      105266                      36 bp
DEFINITION Sequence 27 from Patent EP 0251446.
ACCESSION 105266
VERSION    105266.1 GI:591195
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS    Wells,J.A., Cunningham,B.C., Caldwell,R.M., Bott,R.R., Estell,D.A.
TITLE      Non-human Carbonyl hydrolase mutants, DNA sequences and vectors
           encoding same and hosts transformed with said vectors
JOURNAL    Patent: EP 0251446-A2 27 07 -JAN-1988;
FEATURES   Location/Qualifiers
           source            1..36
BASE COUNT 7 a          11 c          11 g          7 t
ORIGIN

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Fri Jun 21 14:51:59 2002

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230	10.8	23.5	43	22	AAAC82229	Human retrovirus D
231	10.8	23.5	44	12	AAQ10227	Glucosylase/Proch
232	10.8	23.5	44	18	AAV48055	Rapamycin-dependent
233	10.8	23.5	45	13	AAQ28446	Target gag region
234	10.8	23.5	45	14	AAQ47079	HIV ENV gene PCR p
235	10.8	23.5	45	14	AAQ46670	Duplex cutting RNA
236	10.8	23.5	45	15	AAQ69507	Human cytochrome P
237	10.8	23.5	45	18	AAE63969	Human cytochrome P
238	10.8	23.5	45	20	AAH71257	Test sequence from
239	10.8	23.5	45	22	AAH89160	Murine wild-type d
240	10.8	23.5	46	15	AAQ69552	Human cholesterol
241	10.8	23.5	46	18	AAE63814	Human cholesterol
242	10.8	23.5	46	20	AAH17102	Test sequence from
243	10.8	23.5	46	21	AAQ93168	Human serum albumi
244	10.8	23.5	46	21	AAQ93168	Human serum albumi
245	10.8	23.5	46	22	AAH26138	Primer HRNA contai
246	10.8	23.5	46	22	AAH26138	Collected PCR prim
247	10.8	23.5	47	21	AAV15868	PCR primer sequenc
248	10.8	23.5	47	21	AAE65990	Human map-related
249	10.8	23.5	47	21	AAE67885	Human map-related
250	10.8	23.5	47	21	AAE69196	Human map-related
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253	10.8	23.5	48	11	AAQ93867	Deletion mutant 1/
254	10.8	23.5	48	11	AAQ93867	Human serum albumi
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256	10.8	23.5	48	21	AAE65864	T cell antigen rec
257	10.8	23.5	48	22	AAH26140	Primer BRNA contai
258	10.8	23.5	50	12	AAQ12981	Template linker pr
259	10.8	23.5	50	12	AAQ12981	HIV template linker
260	10.8	23.5	50	18	AAH74431	HIV-1 CDNA amplifi
261	10.8	23.5	50	20	AAH26185	Antisense oligo u
262	10.8	23.5	50	22	AAH34162	Antisense oligonuc
263	10.8	23.5	50	22	AAH34162	Human SNP oligonuc
264	10.6	23.0	15	24	AAH93377	Aldehyde dehydroge
265	10.6	23.0	15	24	AAH93377	Primer for B. subt
266	10.6	23.0	29	14	AAQ90034	Alpha subunit spec
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268	10.6	23.0	29	19	AAH78226	Nucleotide sequenc
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270	10.6	23.0	29	21	AAZ49047	PCR primer for fas
271	10.6	23.0	30	14	AAQ42375	TH3 promoter 3' p
272	10.6	23.0	30	19	AAQ42375	PCR primer TDR3-3'
273	10.6	23.0	30	22	AAH34137	Primer #8. Uniden
274	10.6	23.0	31	19	AAV14420	Target sequence #1
275	10.6	23.0	31	19	AAV13028	Mycobacterium para
276	10.6	23.0	31	20	AAH26345	PCR primer used to
277	10.6	23.0	31	23	ABR06702	Human NCOO DNAzyme
278	10.6	23.0	32	20	AAQ06966	P. daeiae rgha oli
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280	10.6	23.0	33	15	AAQ70256	Bacteriophage T4 g
281	10.6	23.0	33	16	AAQ70256	M. tuberculosis DE
282	10.6	23.0	33	22	AAH29167	Rhodococcus rhodoc
283	10.6	23.0	33	22	AAH77372	Human negative reg
284	10.6	23.0	33	22	AAH77372	Human ubiquitin-11
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288	10.6	23.0	33	22	AAH77372	Human ubiquitin-11
289	10.6	23.0	33	22	AAH77372	Human ubiquitin-11
290	10.6	23.0	33	22	AAH77372	Human ubiquitin-11
291	10.6	23.0	33	22	AAH77372	Human ubiquitin-11
292	10.6	23.0	33	22	AAH77372	Human ubiquitin-11
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Fri Jun 21 14:52:00 2002

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 c 974 9.8 21.3 26 17 AAT32106
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 c 978 9.8 21.3 26 20 AAV80009
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 c 989 9.8 21.3 27 13 AAQ29734
 c 990 9.8 21.3 27 14 AAQ42300
 c 991 9.8 21.3 27 22 AAH91471
 c 992 9.8 21.3 28 13 AAQ31029
 c 993 9.8 21.3 28 16 AAQ92514
 c 994 9.8 21.3 28 16 AAQ92514
 c 995 9.8 21.3 28 19 AAX09380
 c 996 9.8 21.3 28 19 AAV66891
 c 997 9.8 21.3 28 19 AAV37308
 c 998 9.8 21.3 28 21 AAA13320
 c 999 9.8 21.3 28 21 AAZ56054
 1000 9.8 21.3 29 19 AAV11290

ALIGNMENTS

RESULT 1
 ID AAN91962/c
 XX AAN91962 standard; DNA; 50 BP.

XX AC AAN91962;
 XX DT 13-APR-1990 (first entry)

XX DE Complementary strand of the Neisseria gonorrhoeae Tem-1 beta lactamase
 XX DE gene combined with lla2c amplifier probe.
 XX KW Neisseria gonorrhoeae; beta lactamase Tem-1; capture probe;
 XX KW amplifier probe lla2c; temkit21.25; TEM-1NH assay.

XX OS Neisseria gonorrhoeae.

XX PH Key Location/Qualifiers
 FT misc_feature 1..30
 FT /*tag- a

FT /*capture probe"
 FT misc_feature 31..50
 FT /*tag- b
 FT /*lla2c amplifier probe"

XX WO8903891-A.

PD 05-MAY-1989.
 XX 14-OCT-1988; 88WO-US03644.
 PF 30-SEP-1988; 88US-0252638, US-109282.
 XX (CHIR-) CHIRON CORP.
 PA Urdea MS, Warner B, Running JA, Kolberg JA, Clyne JM;
 PI Sanchez-Pescador R;
 PI WPI; 1989-150787/20.
 DR Nucleic acid multimer for hybridisation assays
 XX - having single-stranded oligo-nucleotide units
 XX capable of binding specifically to sequences of interest.
 XX Fig 10-2; ; 112pp; English.
 XX Partial nucleotide sequences of the capture and amplifier probes used in
 XX the TEM-1NH assay. The capture probe is complementary to the coding
 XX strand of N. gonorrhoeae Tem-1 beta lactamase gene. It is called
 XX temkit21.25.
 XX Sequence 50 BP; 22 A; 10 C; 12 G; 6 T; 0 other;
 SQ

Query Match 31.7%; Score 14.6; DB 10; Length 50;
 Best Local Similarity 50.0%; Pred. No. 7.4e+02;
 Matches 17; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 cnggtgacnctcaatnnntnnnncantngc 36
 |||||
 Db 46 CGGTCTCTATGCTAAATTTTTCGGCATTTTC 13

RESULT 2
 ID ABK04133 standard; RNA; 38 BP.
 XX ABK04133;
 XX 12-MAR-2002 (first entry)
 XX Human NOGO Hammerhead ribozyme substrate sequence #340.
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US04273.
 XX 11-FEB-2000; 2000US-181797P.
 XX 28-FEB-2000; 2000US-185516P.
 XX 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA

XX (BLAT/) BLATT L.
PA (MCSM/) MCSWIGGEN J.
PA (CHOM/) CHOMRIRA B M.

PI Blatt L., MCSwigen J., Chowrira BK;
DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neutrite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
PT and central nervous system injury

PS Claim 89; Page 71; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neutrite growth inhibitor gene (NOSD).
CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) or an enzyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN
CC motif) or an ameyzyme (cleaving RNA with an NNN triplet), a zincyme
CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
CC to cleave RNA of CD20 in the presence of a divalent cation that is
CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targeting
CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NH), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoxa (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopenia, and inflammatory arthropathy. The NOSD-targetting
CC nucleic acid is used to cleave RNA of the NOSD gene in the presence of a
CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NOSD activity of the cell and
CC treat a patient having a condition associated with the level of NOSD. The
CC treatment may further comprise the use of one or more therapies.
CC In particular, the NOSD-targetting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Gauffeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOSD expression. The
CC present sequence is a substrate sequence for a nucleic acid of the
CC invention based on the human NOSD sequence.

XX Sequence 38 BP; 13 A; 7 C; 10 G; 8 U; 0 other;

SQ

Query Match 30.4%; Score 14; DB 23; Length 38;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 12; Conservative 5; Mismatches 19; Indels 0; Caps 0;

OY 11 acntcaaatnmtngancantcunggnagat 46
||| : ||| : ||| : ||| : ||| :
DB 1 acaugcaacugaugaggcgguaggcggaagaau 36

RESULT 3
AAZ66661/C
ID AAZ66661 standard; DNA: 47 BP.
AAZ66661:
10-SEP-2001 (first entry)
Human map-related biallelic marker SEQ ID NO:1008.
DE Human genome; biallelic marker; high density disequilibrium map;
XK genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW

XX	haplotyping; hybridisation; identification; characterisation;
KM	diagnosis; single nucleotide polymorphism; SNP; ds.
OS	Homo sapiens.
FM	Key
FT	variation
FT	/tag= a
FT	/standard_name= "single nucleotide polymorphism"
XX	
PN	M09954500-A2.
XX	
PD	28-OCT-1999.
XX	
PF	21-APR-1999; 99MO-ID0822.
XX	
PR	21-APR-1998; 98US-0082614.
PR	23-NOV-1998; 98US-0109732.
XX	(GEST) GENSET.
PA	
PI	Cohen D, Blumenfeld M, Chumakov I;
XX	
DR	WPI: 2000-013267/01.
XX	
PT	Novel biallelic markers used to construct a high density disequilibrium
PT	map of the human genome -
XX	
PS	Claim 1; Page 445; 2745pp; English.
XX	
CC	AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC	invention, which contain a polymorphic base at position 24 of their
CC	nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC	primers for the biallelic markers. The biallelic markers of the
CC	primers have a variety of uses: they can be used for high density
CC	invention of the human genome, and in complex association studies and
CC	mapping of disease states. Compositions and methods of the invention can also
CC	be useful for the identification of the targets for the development of
CC	pharmaceutical agents and diagnostic methods, as well as the
CC	characterisation of the differential efficacious responses to and side
CC	effects from pharmaceutical agents acting on a disease as well as other
CC	treatment.
CC	N.B. the SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC	and 3367, are not actually given a sequence in the Sequence Listing
CC	from the present invention.
XX	
XX	Sequence 47 BP; 20 A; 6 C; 6 G; 15 T; 0 other;
SEQ	
OY	11 acntcnaatnmtngacnttgcgagcgatcat 46
DB	
	47 ACTTAATCATCAGACGAGTATTCTCAAGTCAGTGATTAT 12
RESULT 4	
AAZ68854	
ID	AAZ68854 standard; DNA; 47 BP.
AC	
XX	AAZ68854;
DT	
XX	10-SEP-2001 (first entry)
DE	
XX	Human map-related biallelic marker SEQ ID NO:3207.
XX	
XX	Human genome; biallelic marker; high density disequilibrium map;
KM	genomic map; haplotype; phenotype; polymorphic base; genotyping;
KM	haplotyping; hybridisation; identification; characterisation;
KM	diagnosis; single nucleotide polymorphism; SNP; ds.

XX XX Homo sapiens. Location/Qualifiers
OS XX Key replace(24,T)
PF XX variation /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO9954500-A2.
PN
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
PR
XX 23-NOV-1998; 98US-0109732.
PR
XX (GSET) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX WPI: 2000-013267/01.
DR
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome
DT
XX
XX Claim 3; Page 914; 2745pp; English.
FS
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
XX Sequence 47 BP; 19 A; 11 C; 9 G; 8 T; 0 other;
SQ

Query Match 30.08; Score 13.8; DB 21; Length 47;
Best Local Similarity 51.7%; Pred. No 1.8e+03;
Matches 15; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 14 tcaaatnnnnngcattngcngnag 42
| ||| || || || || ||
Db 2 taaatacatgaccacaattagcggcag 30

RESULT 5
AA30308/C
ID AA30308 standard; DNA; 48 BP.
XX
XX AA30308;
AC
XX
XX 11-SEP-2000 (first entry)
DT
XX M. tuberculosis Cu, Zn Superoxide dismutase, SOD, gene fragment.
DE
XX Cu, Zn superoxide dismutase; antibody; tuberculosis; enzyme;
XX superoxide radical; macrophage; sodC; bacterium detection; ds.
KW
XX Mycobacterium tuberculosis.
OS
XX WO200029017-A1.
PN

New transcription regulating fragments of hexokinase II DNA conty.
PT response element - and methods for diagnosis or treatment of
PT neoplasias that over-express hexokinase II and for regulating
PT glycolysis

Claim 1; Fig 11; 104pp: English.

XX The present sequence represents a segment of the hepatoma AS-30D type
CC II hexokinase promoter region. Response elements (transcription factor
CC binding site) in this fragment may consist of all or part of the
CC present sequence. AS-30D is a new isolated hexokinase II. The present
CC DNA fragment is capable of regulating transcription of a downstream
CC open reading frame and contains at least one response element. The
CC present DNA fragment may be coupled to a reporter gene and used to
CC screen for potential drugs that affect regulated transcription of
CC tumour hexokinase II. Alternatively it may be coupled to a toxic gene
CC and used to treat cells that over-express hexokinase II, such as those
CC present in patients with cancer. It may also be used in gene therapy
CC to treat diabetes. The DNA fragment increases glycolysis in cells and
CC to treat homologous or heterologous protein. Probes of the DNA fragment
CC are used in the method for diagnosing a neoplasm that over-expresses
CC hexokinase. The new response elements are active only in tumours, not
CC in normal cells.

XX Sequence 49 BP; 9 A; 13 C; 14 G; 13 T; 0 other;
SO

Query Match 29.1%; Score 13.4; DB 18; Length 49;
Best Local Similarity 45.9%; Pred. No. 36+03;
Matches 17; Conservative 0; Mismatches 20; Indels 0; Gaps

OY 5 ggtgcacatcnaatnnntnmgncantngcngna 41
||||| | | | | | | | | |
DB 44 GGTCGCACTACCTTATCAGACCCTTGCGGGCA 8

RESULT	8
AAV08603/c	
ID	AAV08603 standard; DNA; 49 BP.
XX	
XX	AAV08603;
XX	
DT	18-FEB-1999 (first entry)
XX	
DE	PCR primer for human haemoglobin mutant.
XX	
XX	Haemoglobin; mutant; human; substitute blood product; synthetic blood
KW	beta chain; PCR primer; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
XX	US5827693-A.
PD	27-OCT-1998.
XX	
XX	07-JUN-1995; 95US-0484686.
XX	
PR	29-APR-1992; 92US-0876290.
PR	16-APR-1990; 90US-0309918.
PR	14-NOV-1990; 90US-0614359.
PR	12-APR-1991; 91US-0684611.
PR	29-DEC-1994; 94US-0368407.
PR	07-JUN-1995; 95US-0484686.
XX	
PA	(APEX-) APEX BIOSCIENCE INC.
PI	Bajwa W, Bonaventura J, De Angelo J, Motwani NM;
XX	
DR	WPI; 1998-593993/50.
XX	
XX	Recombinant expression of globin chains - and variants in yeast,
PT	useful as substitutes for natural blood required for oxygen carriage

Example 25: Fig 51: 144pp; English.

The present invention relates to a substantially pure globin chain which is free of erythrocyte membrane components, *Escherichia coli* endotoxins and mammalian cell components. The globin combined with a source of heme is useful for producing hemoglobin, which in turn is useful as physiological oxygen carrier, blood substitute solutions and in plasma expanders or in applications where physiological oxygen carrier.

10 pp. 12 A. 14 C. 12 G. 11 T; 0 other;

Query Match	28.7%	Score 13.2;	DB 22;	Length 45;
Best Local Similarity	42.9%	Pred. No. 3.7e+03;		
Matches 18; Conservative	0;	Mismatches 24;	Indels	

QY
3 cnggtggaacntcnaatnnntnnnngncanttngcnggnagt 44

RESULT 10
ABA10848
DNA: 49 BP.

XX
26-FEB-2002 (first entry)

AA

XX Gene sorting; PCR primer; disease diagnosis; disease analysis;
KW Gene sorting; PCR primer; disease diagnosis; disease analysis;
KW Gene sorting; PCR primer; disease diagnosis; disease analysis;
KW Gene sorting; PCR primer; disease diagnosis; disease analysis;

synthetic.

WO200175180-A2.

XX 11-OCT-2001..
PD
XX 23-MAR-2001. 2001WO-11S09392.
BT

30-MAR-2000: 2000US-0538709.

XX
CORP., ORT ENTERPRISES LTD.
DZ[illegible]

PI Ulanovsky L, Mugasimangalam

2000

DR WPI; 2001-626451/72.

XX Sorting genes into non-redundant groups, useful e.g. for gene
PT isolation, diagnosis and in gene therapy, by amplifying cDNA fragments
PT attached to selective adaptors -

Example 2: Fig 18: 67pp; English.

The present invention relates to a method for sorting genes. The method comprises producing first double stranded (ds) cDNA from mRNA by reverse transcription using a poly-T primer. The ds cDNA is then digested with a restriction enzyme that generates cohesive ends with overhanging single stranded sequence containing a constant number of nucleotides, and the digestion products are ligated to a set of ds DNA oligonucleotide adaptors. Each adaptor has at one end, a sequence complementary to a possible overhang and the other end a primer-template sequence specific for the adaptor complementary sequence, and between these two ends the same sequence is present for all adaptors. The ligated cDNA molecules are amplified in separate PCR assays, using for each a primer that anneals to polyT and a second primer, from a set that anneals to the cDNA specific primer-template sequences. Amplicons are finally sorted into non-redundant groups defined by the specific primer that annealed to the primer-template sequence and thus primed PCR. The method is useful for producing a collection of non-redundant cDNA groups, especially where

QY 14 tcnatnnntnngncantngc 30

Db 9 gtcaattgcaaggaagta 27

us-09-509-234c-1_1000_1045.primer.rng

Fri Jun 21 14:52:00 2002

XX 10-MAY-1999; 99JP-0128674.
PF
XX 10-MAY-1999; 99JP-0128674.
PR
XX (SAKA) OTSUKA PHARM CO LTD.
PA
XX WPI; 2001-184995/19.
XX P-PSDB; AAB45781.
DR
XX A ceramide-combining peptide
PT
XX Disclosure; Page 8; 10pp; Japanese.
PS
XX This invention describes novel ceramide-combining peptides. Such peptides
CC are useful as a tool for elucidating the molecular mechanism of cell
CC signal-transfer and various cell functions and life phenomena accompanied
CC to it.
CC
XX Sequence 45 BP; 5 A; 5 C; 15 G; 20 T; 0 other;
SQ

Query Match 27.8%; Score 12.8; DB 22; Length 45;
Best Local Similarity 43.6%; Pred. No. 5.7e+03;
Matches 17; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Oy 6 gtggnaatcnaatnnnnnncantngcngnagnt 44
| | | | | | | | | | | | | | | | | | | |
Db 4 gtggggcgctattttttatgtgttactttttcgatgat 42

RESULT 15
AAZ68716/c
ID AAZ68716 standard; DNA; 47 BP.
XX
AC AAZ68716;
XX
XX 10-SEP-2001 (first entry)
DT
XX Human map-related biallelic marker SEQ ID NO:3067.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
OS
XX
XX Location/Qualifiers
FH replace(24.G)
FT /tag=a
FT /standard_name="single nucleotide polymorphism"
FT
XX WO9954500-A2.
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-1B00822.
XX
XX 21-APR-1998; 98US-0082614.
XX 23-NOV-1998; 98US-0109732.
PR
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 3; Page 884; 2745pp; English.
XX
XX

RESULT 13
AAH41274
ID AAH41274 standard; DNA; 41 BP.
XX
XX AAH41274;
AC
XX 31-AUG-2001 (first entry)
DT
XX Human prolipoprotein signal peptide 14 probe #1.
DE
XX Human; cytostatic; anti-HIV; immunogenic; antiinflammatory; probe;
XX prolipoprotein signal peptide 14; malignant tumour; haemopathy;
KW HIV infection; immunological disease; inflammation; ss.
XX
XX Homo sapiens.
OS
XX WO200140299-A1.
XX
XX 07-JUN-2001.
PD
XX 27-NOV-2000; 2000WO-CN00514.
PF
XX 30-NOV-1999; 99CN-0124174.
PR
XX (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-374794/39.
DR
XX Human prolipoprotein signal peptide 14 and encoded polynucleotide,
XX applicable in diagnosis and treatment of malignant tumor, hemopathy,
PT HIV infection, immunological diseases and various inflammation
PT
XX Example 6; Page 15; 36pp; Chinese.
PS
XX The present invention relates to human prolipoprotein signal peptide 14
XX and coding sequence (see AAH41269 and AAB91175). The signal peptide and
CC coding sequence are useful in the diagnosis and treatment of malignant
CC tumour, haemopathy, HIV infection, immunological diseases and various
CC inflammation. The present sequence is a probe, which was used in an
CC inflammation from the present invention.
XX
XX Sequence 41 BP; 15 A; 6 C; 8 G; 12 T; 0 other;
SQ

Query Match 27.8%; Score 12.8; DB 22; Length 41;
Best Local Similarity 50.0%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Oy 9 gnaatcnaatnnnnnncantngc 36
| | | | | | | | | | | | | | | | | | | |
Db 4 gtaaatcagatgattagagacatttcg 31

RESULT 14
AAF25923
ID AAF25923 standard; DNA; 45 BP.
XX
XX AAF25923;
AC
XX 19-APR-2001 (first entry)
DT
XX Ceramide affinity peptide CerBP#21 encoding DNA SEQ ID 17.
XX
XX Ceramide; cell signal transfer; cell function; ds.
XX
XX Synthetic.
OS
XX JP2000319296-A.
XX
XX 21-NOV-2000.
PD

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ65979 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SO Sequence 47 BP; 15 A; 7 C; 8 G; 17 T; 0 other;

Query Match	27.8%	Score 12.8;	DB 21;	Length 47;
Best Local Similarity	43.6%	Pred. No. 5.8e+03;		
Matches 17; Conservative		0; Mismatches 22;	Indels 0;	Gaps 0;

QY 6 gtagnacntcaatmtntnngncanttngcngnagt 44
||| ||| | ||| ||| |||
Db 44 GTGTAAGTGTAAACACACGAAATCTATTTCACGGAAGTT 6

Search completed: June 20, 2002, 23:09:49
Job time: 30154 sec

831	9.6	20.9	37	4	US-09-350-399-65	Sequence 65, Appl	c 904	9.6	20.9	50	1	US-08-111-389-20	Sequence 20, Appl
832	9.6	20.9	37	5	PCT-US93-11198-509	Sequence 509, App	c 905	9.6	20.9	50	1	US-08-111-389-352	Sequence 352, App
833	9.6	20.9	37	5	PCT-US93-11198-513	Sequence 513, App	c 906	9.6	20.9	50	1	US-08-111-389-534	Sequence 534, App
834	9.6	20.9	37	5	PCT-US93-11198-515	Sequence 515, App	c 907	9.6	20.9	50	1	US-08-111-389-546	Sequence 546, App
835	9.6	20.9	37	6	5240845-63	Patent No. 5240845	c 908	9.6	20.9	50	1	US-08-207-901-77	Sequence 77, Appl
c 836	9.6	20.9	37	6	5240845-65	Patent No. 5240845	c 909	9.6	20.9	50	1	US-08-123-936-20	Sequence 20, Appl
c 837	9.6	20.9	37	6	5240845-65	Patent No. 5240845	c 910	9.6	20.9	50	1	US-08-123-936-352	Sequence 352, App
c 838	9.6	20.9	38	2	US-08-709-923-5	Sequence 5, Appl1	c 911	9.6	20.9	50	1	US-08-123-936-534	Sequence 534, App
c 839	9.6	20.9	39	1	US-08-086-4288-123	Sequence 123, App	c 912	9.6	20.9	50	1	US-08-123-936-546	Sequence 546, App
c 840	9.6	20.9	39	2	US-08-468-570-123	Sequence 123, App	c 913	9.6	20.9	50	2	US-08-475-2288-20	Sequence 20, Appl
c 841	9.6	20.9	39	2	US-08-290-6655-227	Sequence 227, App	c 914	9.6	20.9	50	2	US-08-475-2288-352	Sequence 352, App
c 842	9.6	20.9	39	3	US-08-799-897-3	Sequence 3, Appl1	c 915	9.6	20.9	50	2	US-08-475-2288-534	Sequence 534, App
c 843	9.6	20.9	39	3	US-08-470-535-17	Sequence 17, Appl	c 916	9.6	20.9	50	2	US-08-475-2288-546	Sequence 546, App
c 844	9.6	20.9	39	3	PCT-US95-10398-227	Sequence 227, App	c 917	9.6	20.9	50	3	US-08-086-080A-20	Sequence 20, Appl
c 845	9.6	20.9	40	1	US-08-045-806-8	Sequence 8, Appl1	c 918	9.6	20.9	50	3	US-08-482-080A-352	Sequence 352, App
c 846	9.6	20.9	40	1	US-08-366-0518-8	Sequence 8, Appl1	c 919	9.6	20.9	50	3	US-08-482-080A-534	Sequence 534, App
c 847	9.6	20.9	40	2	US-08-938-858-3	Sequence 11, Appl	c 920	9.6	20.9	50	4	US-08-972-927-74	Sequence 74, Appl
c 848	9.6	20.9	40	2	US-08-857-946-9	Sequence 3, Appl1	c 921	9.6	20.9	50	4	US-08-849-567A-77	Sequence 77, Appl
c 849	9.6	20.9	40	3	US-08-970-740-49	Sequence 49, Appl	c 922	9.6	20.9	50	5	PCT-US93-12388-352	Sequence 352, App
c 850	9.6	20.9	40	3	US-08-721-4588-60	Sequence 60, Appl	c 923	9.6	20.9	50	5	PCT-US93-12388-534	Sequence 534, App
c 851	9.6	20.9	41	1	US-08-268-6798-6	Sequence 6, Appl1	c 924	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 852	9.6	20.9	41	1	US-08-231-342-9	Sequence 9, Appl1	c 925	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 853	9.6	20.9	41	1	US-09-025-7698-111	Sequence 11, App	c 926	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 854	9.6	20.9	42	1	US-08-045-264A-5	Sequence 5, Appl1	c 927	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 855	9.6	20.9	42	2	US-08-428-257A-55	Sequence 55, Appl	c 928	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 856	9.6	20.9	42	2	US-08-194-981E-63	Sequence 63, Appl	c 929	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 857	9.6	20.9	42	4	US-09-390-577-7	Sequence 7, Appl1	c 930	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 858	9.6	20.9	42	4	US-09-390-577-20	Sequence 20, Appl	c 931	9.6	20.9	50	5	PCT-US93-12388-546	Sequence 546, App
c 859	9.6	20.9											

ALIGNMENTS

APPLICANT: MUTHAIAH, NARAYANA
 APPLICANT: Bajwa, Wajeeh
 TITLE OF INVENTION: Expression of Recombinant Hemoglobin and
 TITLE OF INVENTION: Hemoglobin Variants in Yeast
 NUMBER OF SEQUENCES: 71

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MEDIUM TYPE: Floppy disk

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Query Match	28.7%;	Score 13.2;	DB 1;	Length 49;
Best Local Similarity	42.9%;	Pred. No. 3.8e+02;		

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,160B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-044-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-463-160B-57

Query Match 28.7%; Score 13.2; DB 4; Length 49;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 cngtggacnctcaatnntnngcancntngcngnagnt 44
DB 47 CTCGTGCACGACTGAGCTTATGCAATTGATCCAACT 6

RESULT 4
PCT-US91-02568-13/C
GENERAL INFORMATION:
SEQUENCE 13, Application PC/TUS9102568
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini M
APPLICANT: Bajwa, Waheed
TITLE OF INVENTION: Expression Of Recombinant Hemoglobin
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02568
FILING DATE: 19910415
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-008-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090

TELEFAX: 212 869-9741
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US91-02568-13

Query Match 28.7%; Score 13.2; DB 5; Length 49;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 cngtggacnctcaatnntnngcancntngcngnagnt 44
DB 47 CTCGTGCACGACTGAGCTTATGCAATTGATCCAACT 6

RESULT 5
US-08-488-113B-39/C
SEQUENCE 39, Application US/08488113B
PATENT NO. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Stankula, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs

us-09-509-234c-1_1000_1045.primer.rni

Fri Jun 21 14:52:00 2002

US-08-488-113B-39

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA

Query Match 28.3%; Score 13; DB 1; Length 33;
 Best Local Similarity 56.5%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnnnnngncantngc 36
 ||||| | |||||
 Db 23 TCAATGACTGTGCACAGTTGSC 1

US-08-477-484B-39/c

Sequence 39, Application US/08477484B
 Patent No. 5756699

GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 169
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,484B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA

US-08-477-484B-39

Query Match 28.3%; Score 13; DB 1; Length 33;
 Best Local Similarity 56.5%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 tcnaatnnnnnngncantngc 36
 ||||| | |||||
 Db 23 TCAATGACTGTGCACAGTTGSC 1

US-08-646-360-39/c

Sequence 39, Application US/08646360
 Patent No. 5837491

GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-646-360-39

Query Match 28.3%; Score 13; DB 2; Length 33;

Db 23 TCAATGACTGTGGACAGTTGCC 1

us-09-509-234c-1_1000_1045.primer.rni

Fri Jun 21 14:52:00 2002

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RESULT 10
US-08-596-387B-104
; Sequence 104, Application US/08596387B
; Patent No. 5869270
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,387B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09816
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; US-08-596-387B-104

Query Match 27.4%; Score 12.6; DB 2; Length 45;
Best Local Similarity 48.4%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3 cnggtggnacntcnaatnnnnnngcattt 33
Db 5 CAGGTGGCACCTCCAGACACCCAGGCGCTTT 35

RESULT 11
US-09-067-615-104
; Sequence 104, Application US/09067615
; Patent No. 6309645
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
```

```
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dade International, Inc.
STREET: 1717 Deerfield Road
CITY: Deerfield
STATE: Illinois
COUNTRY: USA
ZIP: 60015
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,615
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,387
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STR-4665-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-09-067-615-104

Query Match 27.4%; Score 12.6; DB 4; Length 45;
Best Local Similarity 48.4%; Pred. No. 7.5e+02;
Matches 15; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3 cnggtggnacntcnaatnnnnnngcattt 33
Db 5 CAGGTGGCACCTCCAGACACCCAGGCGCTTT 35

RESULT 12
PCT-US95-09816A-104
; Sequence 104, Application PC/TUS9509816A
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; APPLICANT: Rhode, Peter R.
; APPLICANT: Widanz, Jon A.
; APPLICANT: Grammer, Susan
; APPLICANT: Edwards, Ana C.
; APPLICANT: Chavalliaz, Pierre-Andre
; APPLICANT: Jiao, Jin-An
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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us-09-509-234c-1_1000_1045.primer.mri

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09816A
FILING DATE: 31-JUL-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STR-4665-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEFAX: (708) 267-5376
INFORMATION FOR SRO. ID NO.: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
PCT-US95-09816A-104

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Query Match	Score 12.6	DB 5	Length 45
Best Local Similarity	48.4%	Pred. No. 7	Se2+2
Matches 15	Conservative	0	Mismatches 16
			Indels 0
			Gaps 0
OY	3 cnggtgnaentcaatnmtntmgcancit	33	
Db	5 CAGGTGCACCTCCAGACACCCACGAGCCTT	35	

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RESULT 13
RE34606-8
;PATENT NO. RE34,606
;APPLICANT: ESTELL, DAVID A.;WELLS, JAMES A.;BOTT,
;RICHARD R.
;TITLE OF INVENTION: MODIFIED ENZYMES AND METHODS FOR
;MAKING SAME
;NUMBER OF SEQUENCES: 27
;CURRENT APPLICATION NUMBER:
;APPLICATION NUMBER: US/07/556,918
;FILING DATE: 20-JUL-1990
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 614,612
;FILING DATE: 29-MAY-1984
;SEQ ID NO.:8
;LENGTH: 48
RE34606-8

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Query Match	27.4%	Score 12.6	DB 6	Length 48
Best Local Similarity	46.9%	Pred. Mo 7	7e+02	
Matches	15	Conservative	0	Mismatches 17, Indels 0, Gaps
QY	8	gymacntcnaatnnatnnngncantngcng	39	
DB	10	ggractcgaatgacatctccgcacgttgcg	41	

RESULT 14
US-08-088-658-46
; Sequence 46, Application US/08088658
; Patent No. 5541625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole

APPLICANT: Espholm, Michael
 APPLICANT: Nielsen, Peter E.
 APPLICANT: Berg, Rolf H.
 APPLICANT: M llaard, Niels E.
 TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
 TITLE OF INVENTION: NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/088,658
 FILING DATE: 19930702
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/054,363
 FILING DATE: 26-APRIL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Luccl, Joseph
 REGISTRATION NUMBER: 33,307
 REFERENCE/DOCKET NUMBER: ISIS-1052
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

Query Match	27.08;	Score 12.4;	DB 1;	Length 50;
Best Local Similarity	4.28;	Peed. No. 1e+03;		
Matches 16;	Conservative 0;	Mismatches 21;	Indels 0;	Gaps 0;
Qy	8	ggaacatcnaactmntnmgacatttngcngcnaagt	44	
Db	12	GAACAGCATATTTCTTTAAATTTAGCGGAGAAAT	48	

RESULT 15
 US-08-471-907A-46
 Sequence 46, Application US/08471907A
 Patent No. 5986053
 GENERAL INFORMATION:
 APPLICANT: Ecker, David J.
 APPLICANT: Buchardt, Ole
 APPLICANT: Echolm, Michael
 APPLICANT: Nielsen, Peter E.
 APPLICANT: Berg, Rolf H.
 APPLICANT: M lligard, Niels E.
 TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
 TITLE OF INVENTION: NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053rls
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:

us-09-509-234c-l_1000_1045.primer.rni

Fri Jun 21 14:52:00 2002

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/088,658
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lucchi, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 50
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-471-907A-46

Query Match 27.0%; Score 12.4; DB 2; Length 50;
Best Local Similarity 43.2%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 8 ggnacatcnaatnnnnnngcattngcngnagnt 44
| | | | | | | | | | | | | | | | | |
DB 12 GAAACAGCATATTTCTTTTAAATATTAGCAGGAGAT 48

Search completed: June 20, 2002, 23:43:22
Job time: 5182 sec

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c 384 9.4 20.4 49 9 A1689495
c 385 9.4 20.4 49 9 A1758169
c 386 9.4 20.4 49 12 A2593107
c 387 9.4 20.4 49 12 A2762215
c 388 9.4 20.4 50 9 A1000832
c 389 9.4 20.4 50 9 A102381
c 390 9.4 20.4 50 9 A102853
c 391 9.4 20.4 50 9 A102991
c 392 9.4 20.4 50 9 A103451
c 393 9.4 20.4 50 9 A103473
c 394 9.4 20.4 50 9 A103486
c 395 9.4 20.4 50 9 A103490
c 396 9.4 20.4 50 9 A103568
c 397 9.4 20.4 50 9 A103868
c 398 9.4 20.4 50 9 A103991
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c 400 9.4 20.4 50 9 A104380
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c 402 9.4 20.4 50 9 A105172
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c 412 9.4 20.4 50 9 A107431
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c 414 9.4 20.4 50 9 A1783902
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c 417 9.4 20.4 50 10 B183115
c 418 9.4 20.4 50 10 N26705
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c 422 9.2 20.0 26 12 A2825865
c 423 9.2 20.0 29 12 A0025665
c 424 9.2 20.0 30 10 B1392665
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c 433 9.2 20.0 31 10 B1394319
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c 457 9.2 20.0 33 10 B1392886
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c 462 9.2 20.0 33 10 B1393822
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c 486 9.2 20.0 37 12 TA380C04P
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c 504 9.2 20.0 41 10 C21197
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c 506 9.2 20.0 42 9 A0060450
c 507 9.2 20.0 42 10 D20693
c 508 9.2 20.0 42 12 A2378086
c 509 9.2 20.0 42 12 A2458289
c 510 9.2 20.0 42 12 A2771653
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c 516 9.2 20.0 43 9 A1971753
c 517 9.2 20.0 43 12 A0025179
c 518 9.2 20.0 43 12 A2346730
c 519 9.2 20.0 43 12 A2423799
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c 521 9.2 20.0 44 10 D19127
c 522 9.2 20.0 44 10 D68912
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c 525 9.2 20.0 44 12 A2504238
c 526 9.2 20.0 44 12 A2621668
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c 528 9.2 20.0 44 12 BH023762

B1392776 50071-2-1
B1392886 50071-2-2
B1392918 50071-2-3
B1393340 50071-2-9
B1393391 50071-2-9
B1393407 50071-2-9
B1393822 50072-2-1
B1393863 50072-2-1
B1393900 50072-2-1
B1394056 50072-2-1
B1394270 50072-2-2
B1394332 50072-2-3
B1395433 50072-2-9
B1395528 50072-2-9
B1395556 50072-2-9
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A1678784 A1678784
B1393362 50071-2-9
B1395474 50072-2-9
H27469 Y144b05.r1
A2826442 2M0102M07
A2829852 2M0107C16
A2508676 1M0351N07
A2967492 2M0238O22
A155349 T. brucei
A1384342 fb07h06.y
A1634572 t230a01.x
B1393320 602411536
B1782994 T. brucei
A1497720 T. brucei
A1497724 T. brucei
B1782994 602109082
A2394484 1M0158N05
A2421601 1M0199L23
A2514073 1M0360D08
A2764800 1M0561K01
A2938911 2M0197J11
A2345437 1M0080F07
A035761 zk28f07.r
A1790820 v19e12.r
A1590156 t012g08.x
A1679497 A1679497
B1393400 50071-2-9
B1395544 50072-2-9
A2377451 1M0131L17
A2480548 1M0302H12
A2780916 2M0018O12
A2783519 2M0025P13
C21197 HUMGS00221
A1456184 T. brucei
A0060450 HUMGS01669
A2378086 1M0132N07
A2458289 1M0262D14
A2771653 1M0573M15
A2924145 4506.ic27
A0658067 nui7907.s
A1620116 tu92g02.x
A1663481 uk33d07.y
A1683394 tx66f06.x
A1971753 wr07g07.x
A0025179 EF(3)1110
A2346730 1M0082A11
A2423799 1M0203M19
A1256664 ui29h04.y
D19127 MUGS01342
D68912 CELK057D2F
R43593 yc85h01.s1
A2328538 1M0052B24
A2504238 1M0344A23
A2621668 1M0455H11
A2838497 2M0134P08
BH023762 BG02168-3

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT
ORIGIN

12 a 10 c 14 g 14 t

Query Match 31.7%; Score 14.6; DB 12; Length 50;
Best Local Similarity 50.0%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 2 cgggtgacnctcaatnntnnngcancntng 35
||||| | | | | | | | | | | | | | | | | | | | |
Db 17 GCTGTGGATTCGAAACTGATATAGGCACTCTG 50

RESULT 3
AZ800459/c 46 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0058A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0058A04 R, DNA sequence.

ACCESSION
AZ800459
VERSION
AZ800459.1 GI:12952596
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus.

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0058 row: A column: 04
Seq primer: CACACAGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.

TITLE

JOURNAL

COMMENT

FEATURES
source

1. 46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0058A04"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42R; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (g114732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.

BASE COUNT
ORIGIN

9 a 14 c 11 g 12 t

Query Match 31.3%; Score 14.4; DB 12; Length 46;
Best Local Similarity 47.4%; Pred. No. 2e+04;
Matches 18; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 5 gttgagacnctcaatnntnnngcancntngcggna 42
||||| | | | | | | | | | | | | | | | | | | | |
Db 41 GGTGGCACTACCTTATATCTACGACTCAGAGAGCAG 4

RESULT 4
AJ239756 43 bp mRNA linear EST 10-AUG-1999
LOCUS AJ239756 Aspergillus niger ATCC6275 Aspergillus niger cDNA clone
DEFINITION ANO1C03, mRNA sequence.

ACCESSION
AJ239756
VERSION
AJ239756.1 GI:5443747
KEYWORDS
EST.
SOURCE
Aspergillus niger.
ORGANISM
Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE
AUTHORS
1 (bases 1 to 43)
Choi, J.Y., Lee, D.W., Koh, J.S., Kim, J.H., Yang, M.S. and Chae, K.S.
Identification of expressed sequence tags (ESTs) of the highly
transcribed genes in Aspergillus niger
Biotechnol. Lett. 21, 381-384 (1999)

JOURNAL

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BASE COUNT 10 a 8 c 7 g 10 t 8 others
ORIGIN

Query Match 29.6%; Score 13.6; DB 9; Length 43;
Best Local Similarity 51.3%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 3 cnggtgacnctcaatnntnnngcancntngcggna 41
||||| | | | | | | | | | | | | | | | | | | | |
Db 2 CGGCTGTGATTCATCAAGNNAATTNNCCCTTCGCGNA 40

RESULT 5
BF340017 49 bp mRNA linear EST 22-NOV-2000
LOCUS 602036953P1 NCI CGAP_Brn64 Homo sapiens cDNA IMAGE:4184917
DEFINITION 5', mRNA sequence.

ACCESSION
BF340017
VERSION
BF340017.1 GI:11286479
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

Fri Jun 21 14:52:02 2002

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REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9503 row: 1 column: 14
High quality sequence stop: 49.
Location/Qualifiers
1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 5 a 17 c 16 g 11 t
ORIGIN

Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnnnnnnncantt 33
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Db 18 GGTGGTGGCAGCTGTCATTCGCCGCCACTT 49

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 5 a 17 c 16 g 11 t
ORIGIN

Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnnnnnnncantt 33
| ||||| || | | | | | | | | | |
Db 18 GGTGGTGGCAGCTGTCATTCGCCGCCACTT 49

RESULT 6
LOCUS BF340526 49 bp mRNA linear EST 22-NOV-2000
DEFINITION 602037162F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184990
5', mRNA sequence.
ACCESSION BF340526
VERSION BF340526.1 GI:11286988
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 5 a 17 c 16 g 11 t
ORIGIN

Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnnnnnnncantt 33
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Db 18 GGTGGTGGCAGCTGTCATTCGCCGCCACTT 49

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 5 a 17 c 16 g 11 t
ORIGIN

Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnnnnnnncantt 33
| ||||| || | | | | | | | | | |
Db 18 GGTGGTGGCAGCTGTCATTCGCCGCCACTT 49

FEATURES
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/notice="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 5 a 16 c 16 g 12 t
ORIGIN

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/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 5 a 16 c 16 g 12 t
ORIGIN

Query Match 29.6%; Score 13.6; DB 10; Length 49;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 gcggtggnactnaatnnnnnnncantt 33
| ||||| || | | | | | | | | | |
Db 18 GGTGGTGGCAGCTGTCATTCGCCGCCACTT 49

FEATURES
source
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/notice="Vector: pMD22ntv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

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of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT
ORIGIN

9 a 12 c 11 g 9 t

Query Match 29.1%; Score 13.4; DB 12; Length 41;
Best Local Similarity 45.9%; Pred. No. 5.1e+04;
Matches 17; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 6 gtgacatcnaatnntnngcattngcngnag 42
|||||
Db 41 GTGGCAGACGCTTTATCCAGCACTGTGAGCAG 5

RESULT 8
A2489704/c 41 bp DNA linear GSS 05-OCT-2000
LOCUS A2489704
DEFINITION 1M0322L14F Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION A2489704
VERSION A2489704.1 GI:10659714
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 41)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamli, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu

Insert length: 10000 Std Error: 0.00
Plate: 0322 row: L column: 14
Seq primer: CGTGTGAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
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/clone="U06C1M0322L14"
/clone_1lb="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

BASE COUNT
ORIGIN

15 a 7 c 12 g 7 t

Query Match 28.7%; Score 13.2; DB 12; Length 41;
Best Local Similarity 51.7%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 5 ggtgacatcnaatnntnngcatt 33
|||||
Db 30 GTGGTACATCCCTTTATCCAGCACTT 2

RESULT 9
AA933930 46 bp mRNA linear EST 23-JUN-1998
LOCUS AA933930
DEFINITION on94909.s1 Soares-NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1564384 3' similar to SW:UAF4_HUMAN P51826 LAF-4 PROTEIN ;,
mRNA sequence.
ACCESSION AA933930
VERSION AA933930.1 GI:3090198
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
This clone is available royalty-free through ILN; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 570 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1564384"
/clone_1lb="Soares-NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH19W, testis NH7, and B-cell
NCI-GAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo.

FEATURES
SOURCE

BASE COUNT
ORIGIN

9 a 7 c 15 g 15 t

Query Match 28.7%; Score 13.2; DB 9; Length 46;
Best Local Similarity 43.9%; Pred. No. 6.5e+04;
Matches 18; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Best Local Similarity 48.4%; Pred. No. 1.le+05;
Matches 15; Conservative 0; Mismatches 16; Indels 0; Gaps 0

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QY      5 ggtgnaatcnaatnnnnngcancntng 35
          ||||| | | | | | | | |
Db      8 GGTGGACATGCCCTTAATCCAGCACTTGG 38

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RESULT 12
A7769053

Accession	AF169993	43 bp	DNA linear	GSS 16-FEB-2001
LOCUS	AZ769953			
DEFINITION	IM0571E10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0571E10 F, DNA sequence.			

ACCESSION	AZ769953
VERSION	AZ769953.1
KEYWORDS	GSS.
SOURCE	house mouse.

ORGANISM

UNIONISM

AND ANCESTRALITY

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 43)

Dave D. Rowntree & Barbara M. Beccorn, T., Duval, B., Hamill, C.,
Jameson, J.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10Kb

37.114

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
Institute of Utah Genome Center

UNIVERSITY OF UTAH
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5506
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.000
 Plate: 0571 row: E column: 10
 Seq primer: CGGTGTAAACGACGGCGCAT
 Class: plasmid ends
 High quality sequence stop: 43.

FEATURES

Source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0571E10"
clone_lib="mouse 10kb plasmid UUGCIM library"

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Sex⁻mate⁻ E. coli strain XL10-Gold, Tl-resistant, F⁻/lab⁻host⁻ E. coli strain XL10-Gold, Tl-resistant, F⁻/note⁻Vector: pMD42nv; Purified genomic DNA from *musculus* C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repirted with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114753211419b)AD29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT
ORIGIN

7 a 14 c 13 g 9 e

Query Match	27.4%	Score 12.6;	DB 1;	Length 43;
Best Local Similarity	41.9%	Pred. No. 1.2e+05;		
Matches 18; Conservative	0;	Mismatches 25;	Indels 0;	Gaps 0;

Oy 2 gcngtgnacntcnaatnntnmngcantlmgcnagnt 44
||| | | | | | | | |
Db 1 GCAGCGAGTCCCTACTAGTCCTGCAGTCTATGCGCGGACAGT 43

RESULT 13
28437403

AA427403	41 bp	DNA	linear	GSS 03-OCT-2000
LOCUS				
DEFINITION	IM0209P13F Mouse 10kb plasmid	UUGC1M library	Mus musculus	genomic
	clone UUGC1M0209P13 F,	DNA sequence.		

ACCESSION	A427403
VERSION	A2427403.1
KEYWORDS	GSS.
SOURCE	house mouse.

ORGANISM

ORGANISM
MUS MUSCULUS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus
1 (bases 1 to 4)
Barber M., Pearson, T., Dival, B., Hamill, C.,
REFERENCE

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Wells
1400 S. 4th St., 6th Floor, Conoco Center
St. Paul, MN 55402-4000

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.0000
 Plate: 0209 row: P column: 13
 Seq primer: CGTCTGTAAAGACGCCAAT
 Class: plasmid ends
 High quality sequence stop: 41.

FEATURES

Source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06G1M020P13"
/clone_1ib="Mouse 10kb plasmid U06G1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notice="Vector: PMW42nv: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gII47211419b/ARI29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT
ORIGIN

5 a 7 c 11 g 18 t

Fri Jun 21 14:52:02 2002

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 50)

REFERENCE AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: L column: 13
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
1. .50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0012L13"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES source

Query Match 27.0%; Score 12.4; DB 12; Length 41;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 19 tnnntnnngcncantngcngnagnt 44
Db 3 TCTCTGTGTCAGTTTTCAGGGAGTT 28

FEATURES source

RESULT 14
AW768769
LOCUS
DEFINITION
h153a03.x1 NCI_CGAP_Col4 Homo sapiens cDNA clone IMAGE:3004876 3', mRNA linear. EST 04-MAY-2000
RNA sequence.
ACCESSION
AW768769
VERSION
AW768769.1 GI:7700792
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 50)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -400P from Gibco.
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3004876"
/clone_lib="NCI_CGAP_Col4"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.7 Kb. Life Technologies catalog #: 11531-019"

BASE COUNT 20 a 5 c 9 g 16 t
ORIGIN

Query Match 27.0%; Score 12.4; DB 9; Length 50;
Best Local Similarity 43.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 9 gnaactcnaatnnnnngcncantngcngnagnta 45
Db 7 GAATATTAAATTTATTAACTTTCCAGAAAGGTA 43

FEATURES source

RESULT 15
AZ308860/c
LOCUS
DEFINITION
1M0012L13F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0012L13 F, DNA sequence.
ACCESSION
AZ308860
VERSION
AZ308860.1 GI:10349274
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus

BASE COUNT 13 a 14 c 6 g 17 t
ORIGIN

Query Match 27.0%; Score 12.4; DB 12; Length 50;
Best Local Similarity 44.4%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 11 acntcnaatnnnnngcncantngcngnagntat 46
Db 49 AATCAAGGTAAGCTGTCTATTGGTGAAGCTGT 14

Search completed: June 20, 2002, 23:05:46
Job time: 31111 sec

Fri Jun 21 14:52:02 2002

us-09-509-234c-1_1000_1045.primer.rst

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:42:29 ; Search time 1932.32 Seconds
(without alignments)
314.063 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1300_1328
Perfect score: 29
Sequence: 1 nnnnnnataattacagagtttaann 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1797656 segs, 10463368293 residues

Total number of hits satisfying chosen parameters: 663590

Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmb1:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pal:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
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29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	19	65.5	19	6	A97472	A97472 Sequence 28
2	14	48.3	27	6	AX117627	AX117627 Sequence
3	14	48.3	33	6	AR174977	AR174977 Sequence
4	14	48.3	33	6	AR174978	AR174978 Sequence
5	14	48.3	45	6	AR174999	AR174999 Sequence
6	14	48.3	45	6	AR175000	AR175000 Sequence
7	13	44.8	19	6	AX130141	AX130141 Sequence
8	13	44.8	19	6	AX130142	AX130142 Sequence
9	13	44.8	19	6	AX130143	AX130143 Sequence
10	12.8	44.1	24	6	AR043211	AR043211 Sequence
11	12.8	44.1	24	6	AR050529	AR050529 Sequence
12	12.8	44.1	28	6	AR166684	AR166684 Sequence
13	12.8	44.1	35	6	AR12544	AR12544 polypeptide
14	12.8	44.1	35	6	AR97446	AR97446 polypeptide
15	12.8	44.1	39	6	AX117715	AX117715 Sequence
16	12.6	43.4	25	6	AX249110	AX249110 Sequence
17	12.6	43.4	31	6	AX306909	AX306909 Sequence
18	12.6	43.4	32	6	AR032594	AR032594 Sequence
19	12.6	43.4	46	6	I29334	I29334 Sequence 20
20	12.6	43.4	46	6	I91008	I91008 Sequence 20
21	12.6	43.4	46	6	AR038791	AR038791 Sequence
22	12.4	42.8	22	6	AR059677	AR059677 Sequence
23	12.4	42.8	44	6	AR071971	AR071971 Sequence
24	12.4	42.8	44	6	A97447	A97447 Sequence 3
25	12.2	42.1	25	6	AX119427	AX119427 Sequence
26	12.2	42.1	32	6	AR174969	AR174969 Sequence
27	12.2	42.1	39	6	AR048796	AR048796 Sequence
28	12.2	42.1	39	6	AR103237	AR103237 Sequence
29	12.2	42.1	40	6	A83615	A83615 Sequence 44
30	12.2	42.1	40	6	AX249196	AX249196 Sequence
31	12	41.4	31	6	AX040130	AX040130 Sequence
32	12	41.4	20	6	A92003	A92003 Sequence 6
33	11.8	40.7	20	6	AR112676	AR112676 Sequence
34	11.8	40.7	20	6	AX278656	AX278656 Sequence
35	11.8	40.7	24	6	AX155918	AX155918 Sequence
36	11.8	40.7	30	6	AR089388	AR089388 Sequence
37	11.8	40.7	30	6	AR093588	AR093588 Sequence
38	11.8	40.7	45	6	AX049973	AX049973 Sequence
39	11.8	40.7	45	6	AX049974	AX049974 Sequence
40	11.8	40.7	45	6	AX099855	AX099855 Sequence
41	11.8	40.7	45	6	AX099856	AX099856 Sequence
42	11.8	40.7	45	6	AX107691	AX107691 Sequence
43	11.8	40.7	45	6	AX137975	AX137975 Sequence
44	11.8	40.7	45	6	AX137976	AX137976 Sequence
45	11.8	40.7	47	6	AX253569	AX253569 Sequence
46	11.8	40.7	47	6	AX253569	AX253569 Sequence
47	11.8	40.7	50	6	AX147901	AX147901 Sequence
48	11.8	40.7	50	6	AX147930	AX147930 Sequence
49	11.8	40.7	19	6	AX130889	AX130889 Sequence
50	11.6	40.0	21	6	AX011264	AX011264 Sequence
51	11.6	40.0	25	12	AB069280	AB069280 Synthetic
52	11.6	40.0	28	6	AX119423	AX119423 Sequence
53	11.6	40.0	28	6	AX343781	AX343781 Sequence
54	11.6	40.0	32	6	AR146677	AR146677 Sequence
55	11.6	40.0	32	6	AX037504	AX037504 Sequence
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57	11.6	40.0	32	6	AR102833	AR102833 Sequence
58	11.6	40.0	34	6	AR069346	AR069346 Sequence
59	11.6	40.0	34	6	I64563	I64563 Sequence 11
60	11.6	40.0	36	6	AX027858	AX027858 Sequence
61	11.6	40.0	39	6	A27912	A27912 Nucleic ac1
62	11.6	40.0	40	6	A62747	A62747 Sequence 13
63	11.6	40.0	40	6	AX343767	AX343767 Sequence
64	11.6	40.0	47	6	I92614	I92614 Sequence 20
65	11.6	40.0	47	6	AR008503	AR008503 Sequence
66	11.4	39.3	21	6	AR049953	AR049953 Sequence
67	11.4	39.3	21	6	AR099639	AR099639 Sequence
68	11.4	39.3	21	6	I13737	I13737 Sequence 13
69	11.4	39.3	21	6	I34533	I34533 Sequence 27
70	11.4	39.3	21	6	I39803	I39803 Sequence 27
71	11.4	39.3	22	6	AR139341	AR139341 Sequence
72	11.4	39.3	22	6	I13887	I13887 Sequence 1
73	11.4	39.3	22	6	I13887	I13887 Sequence 1

us-09-509-234c-1_1300_1328.primer.rge

Fri Jun 21 14:52:03 2002

c 74	11.4	39.3	22	6	I30457	I30457 Sequence 1	147	11	37.9	44	6	A39217	A39217 Sequence 1
c 75	11.4	39.3	26	6	AX110741	AX110741 Sequence	c 148	11	37.9	44	6	E55471	E55471 Gene expres
c 76	11.4	39.3	30	6	I74335	I74335 Sequence 14	149	11	37.9	45	6	AR139084	AR139084 Sequence
c 77	11.4	39.3	33	6	AX100443	AX100443 Sequence	c 150	11	37.9	45	6	AR147515	AR147515 Sequence
c 78	11.4	39.3	34	6	AK009879	AK009879 Sequence	c 151	11	37.9	45	6	AX214211	AX214211 Sequence
c 79	11.4	39.3	35	6	AR079773	AR079773 Sequence	c 152	11	37.9	45	6	A78547	A78547 Sequence 4
c 80	11.4	39.3	35	6	AR081303	AR081303 Sequence	c 153	11	37.9	50	6	AR016288	AR016288 Sequence
c 81	11.4	39.3	35	6	AX170663	AX170663 Sequence	c 154	11	37.9	50	6	I60387	I60387 Sequence 4
c 82	11.4	39.3	38	6	AX320960	AX320960 Sequence	c 155	10.8	37.2	50	6	A88266	A88266 Sequence 41
c 83	11.4	39.3	38	6	AR058447	AR058447 Sequence	c 156	10.8	37.2	15	6	A88268	A88268 Sequence 41
c 84	11.4	39.3	44	6	AR058448	AR058448 Sequence	c 157	10.8	37.2	15	6	A90233	A90233 Sequence 41
c 85	11.2	38.6	16	6	A86264	A86264 Sequence 41	c 158	10.8	37.2	15	6	A90235	A90235 Sequence 41
c 86	11.2	38.6	16	6	A90231	A90231 Sequence 41	c 159	10.8	37.2	16	6	A04871	A04871 Hexadecamer
c 87	11.2	38.6	17	6	A68193	A68193 Sequence 3	c 160	10.8	37.2	16	6	A04907	A04907 reverse com
c 88	11.2	38.6	17	6	AR043516	AR043516 Sequence	c 161	10.8	37.2	16	6	A06506	A06506 Nucleotide
c 89	11.2	38.6	17	6	AX215158	AX215158 Sequence	c 162	10.8	37.2	16	6	A64269	A64269 Sequence 57
c 90	11.2	38.6	17	6	AX216309	AX216309 Sequence 8	c 163	10.8	37.2	16	6	A64270	A64270 Sequence 58
c 91	11.2	38.6	17	6	I04560	I04560 Sequence 8	c 164	10.8	37.2	16	6	AR102568	AR102568 Sequence
c 92	11.2	38.6	18	6	A04908	A04908 Nucleotide	c 165	10.8	37.2	16	6	AR102569	AR102569 Sequence 59
c 93	11.2	38.6	18	6	AX106833	AX106833 Sequence	c 166	10.8	37.2	16	6	A64271	A64271 Sequence 59
c 94	11.2	38.6	18	6	AX130890	AX130890 Sequence	c 167	10.8	37.2	17	6	AR046203	AR046203 Sequence
c 95	11.2	38.6	18	6	AX130890	AX130890 Sequence	c 168	10.8	37.2	17	6	AR046205	AR046205 Sequence
c 96	11.2	38.6	20	6	A97448	A97448 Sequence 4	c 169	10.8	37.2	17	6	AR046207	AR046207 Sequence
c 97	11.2	38.6	20	6	AX096692	AX096692 Sequence	c 170	10.8	37.2	17	6	AR047286	AR047286 Sequence
c 98	11.2	38.6	21	6	AR077162	AR077162 Sequence	c 171	10.8	37.2	17	6	AR047288	AR047288 Sequence
c 99	11.2	38.6	22	6	AX093523	AX093523 Sequence	c 172	10.8	37.2	17	6	AR047290	AR047290 Sequence
c 100	11.2	38.6	22	6	AX003449	AX003449 Sequence	c 173	10.8	37.2	17	6	AR102570	AR102570 Sequence
c 101	11.2	38.6	23	6	A22444	A22444 MBR primer.	c 174	10.8	37.2	17	6	I53255	I53255 Sequence 99
c 102	11.2	38.6	24	6	AX117180	AX117180 Sequence	c 175	10.8	37.2	17	6	I53257	I53257 Sequence 99
c 103	11.2	38.6	25	6	AX118200	AX118200 Sequence	c 176	10.8	37.2	17	6	I53259	I53259 Sequence 10
c 104	11.2	38.6	25	6	I52003	I52003 Sequence 11	c 177	10.8	37.2	17	6	I53359	I53359 Sequence 20
c 105	11.2	38.6	28	6	I72211	I72211 Sequence 11	c 178	10.8	37.2	17	6	I54340	I54340 Sequence 20
c 106	11.2	38.6	28	6	AX593138	AX593138 Meleagris	c 179	10.8	37.2	17	6	I54342	I54342 Sequence 20
c 107	11.2	38.6	29	11	AX593138	AX593138 Sequence	c 180	10.8	37.2	20	6	AX188413	AX188413 Sequence
c 108	11.2	38.6	30	6	AR142668	AR142668 Sequence 74	c 181	10.8	37.2	21	6	A12545	A12545 polypeptide
c 109	11.2	38.6	30	6	I34988	I34988 Sequence 3	c 182	10.8	37.2	21	6	A65409	A65409 Sequence 1
c 110	11.2	38.6	30	6	I06985	I06985 Sequence 3	c 183	10.8	37.2	21	6	AX326843	AX326843 Sequence
c 111	11.2	38.6	39	6	AR031191	AR031191 Sequence	c 184	10.8	37.2	22	6	AX027192	AX027192 Sequence
c 112	11.2	38.6	39	6	AR088484	AR088484 Sequence	c 185	10.8	37.2	24	6	AX027196	AX027196 Sequence
c 113	11.2	38.6	39	6	I28202	I28202 Sequence 6	c 186	10.8	37.2	24	6	AR073860	AR073860 Sequence
c 114	11.2	38.6	39	6	I39894	I39894 Sequence 6	c 187	10.8	37.2	25	6	AX197169	AX197169 Sequence
c 115	11.2	38.6	40	6	AX020961	AX020961 Sequence	c 188	10.8	37.2	25	6	AX162233	AX162233 Sequence
c 116	11.2	38.6	41	6	AR053398	AR053398 Sequence	c 189	10.8	37.2	25	6	E31890	E31890 Method for
c 117	11.2	38.6	41	6	AR130968	AR130968 Sequence	c 190	10.8	37.2	25	6	I32044	I32044 Sequence 34
c 118	11.2	38.6	44	6	AR034095	AR034095 Sequence	c 191	10.8	37.2	25	6	AX004221	AX004221 Sequence
c 119	11.2	38.6	44	6	AR071317	AR071317 Sequence	c 192	10.8	37.2	26	6	AR142061	AR142061 Sequence
c 120	11.2	38.6	44	6	AX112733	AX112733 Sequence	c 193	10.8	37.2	27	6	AX249915	AX249915 Sequence
c 121	11.2	38.6	44	6	AX225289	AX225289 Sequence	c 194	10.8	37.2	27	6	AX259770	AX259770 Sequence
c 122	11.2	38.6	44	6	AX225302	AX225302 Sequence	c 195	10.8	37.2	27	6	I25346	I25346 Sequence 4
c 123	11.2	38.6	46	6	AX225288	AX225288 Sequence	c 196	10.8	37.2	27	6	I59928	I59928 Sequence 55
c 124	11.2	38.6	46	6	AX225301	AX225301 Sequence	c 197	10.8	37.2	27	6	I86786	I86786 Sequence 55
c 125	11.2	38.6	47	6	AX032553	AX032553 Sequence	c 198	10.8	37.2	27	6	I95811	I95811 Sequence 55
c 126	11.2	38.6	47	6	I30967	I30967 Sequence 16	c 199	10.8	37.2	30	6	AX033635	AX033635 Sequence
c 127	11.2	38.6	50	6	AX165042	AX165042 Sequence	c 200	10.8	37.2	30	6	AR121946	AR121946 Sequence
c 128	11.2	38.6	50	6	AX165042	AX165042 Sequence	c 201	10.8	37.2	30	6	AX203464	AX203464 Sequence
c 129	11.2	38.6	50	6	A67395	A67395 Sequence 20	c 202	10.8	37.2	32	6	A65428	A65428 Sequence 19
c 130	11.2	38.6	50	6	I30965	I30965 Sequence 40	c 203	10.8	37.2	32	6	A65428	A65428 Sequence 20
c 131	11.2	38.6	50	6	I46424	I46424 Sequence 40	c 204	10.8	37.2	34	6	A65428	A65428 Sequence 2
c 132	11.2	38.6	50	6	AX154075	AX154075 Sequence	c 205	10.8	37.2	36	6	AX036004	AX036004 Sequence 18
c 133	11.2	38.6	50	6	A6956	A6956 Sequence 7	c 206	10.8	37.2	38	6	A73302	A73302 Sequence 18
c 134	11.2	38.6	50	6	A39164	A39164 Sequence 12	c 207	10.8	37.2	38	6	AR061043	AR061043 Sequence
c 135	11.2	38.6	50	6	A39223	A39223 Sequence 7	c 208	10.8	37.2	38	6	AR161676	AR161676 Sequence
c 136	11.2	38.6	50	6	BD002560	BD002560 Gene comp	c 209	10.8	37.2	39	6	A36009	A36009 Sequence 8
c 137	11.2	38.6	50	6	AX135259	AX135259 Sequence	c 210	10.8	37.2	41	6	AX040156	AX040156 Sequence
c 138	11.2	38.6	50	6	AX236522	AX236522 Sequence	c 211	10.8	37.2	41	10	MUS1GKRC	MUS1GKRC
c 139	11.2	38.6	50	6	AR166502	AR166502 Sequence	c 212	10.8	37.2	48	6	A36007	A36007 Sequence 6
c 140	11.2	38.6	50	6	A61010	A61010 Sequence 31	c 213	10.8	37.2	48	6	A65431	A65431 Sequence 23
c 141	11.2	38.6	50	6	A61010	A61010 Sequence 31	c 214	10.8	37.2	50	6	I42243	I42243 Sequence 56
c 142	11.2	38.6	50	6	BD008614	BD008614 Antifunga	c 215	10.6	36.6	18	6	AR154171	AR154171 Sequence
c 143	11.2	38.6	50	6	AX109125	AX109125 Sequence	c 216	10.6	36.6	18	6	AR175498	AR175498 Sequence
c 144	11.2	38.6	50	6	A36950	A36950 Sequence 1	c 217	10.6	36.6	19	6	AX130048	AX130048 Sequence
c 145	11.2	38.6	50	6	A39158	A39158 Sequence 6	c 218	10.6	36.6	19	6	AX131495	AX131495 Sequence
c 146	11.2	38.6	50	6	A39158	A39158 Sequence 6	c 219	10.6	36.6	20	6	E51766	E51766 Promoter of

220	10.6	36.6	21	6	AR139979	AR139979 Sequence	C 293	10.4	35.9	20	6	AR162421	AR162421 Sequence
221	10.6	36.6	21	6	AR140298	AR140298 Sequence	C 294	10.4	35.9	20	6	AR162422	AR162422 Sequence
222	10.6	36.6	21	6	AR140576	AR140576 Sequence	C 295	10.4	35.9	20	6	I22601	I22601 Sequence 89
223	10.6	36.6	21	6	AX201210	AX201210 Sequence	C 296	10.4	35.9	20	6	I47426	I47426 Sequence 89
224	10.6	36.6	21	6	AX229680	AX229680 Sequence	C 297	10.4	35.9	21	6	A56969	A56969 Sequence 27
225	10.6	36.6	22	6	AX068220	AX068220 Sequence	C 298	10.4	35.9	21	6	A56668	A56668 Sequence 12
226	10.6	36.6	22	6	AX077179	AX077179 Sequence	C 299	10.4	35.9	21	6	AR035061	AR035061 Sequence
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228	10.6	36.6	23	6	AX226121	AX226121 Sequence	C 301	10.4	35.9	22	6	AX096533	AX096533 Sequence
229	10.6	36.6	24	6	AR037010	AR037010 Sequence	C 302	10.4	35.9	22	6	AX147904	AX147904 Sequence
230	10.6	36.6	24	6	AR049507	AR049507 Sequence	C 303	10.4	35.9	22	6	AX147933	AX147933 Sequence
231	10.6	36.6	24	6	AR171113	AR171113 Sequence	C 304	10.4	35.9	25	6	I46706	I46706 Sequence 68
232	10.6	36.6	24	6	AX068471	AX068471 Sequence	C 305	10.4	35.9	25	6	AX151766	AX151766 Sequence
233	10.6	36.6	25	6	A45241	A45241 Sequence 5	C 306	10.4	35.9	25	6	A33356	A33356 Synthetic P
234	10.6	36.6	25	6	AX155604	AX155604 Sequence	C 307	10.4	35.9	25	6	AR043894	AR043894 Sequence
235	10.6	36.6	25	6	AR171128	AR171128 Sequence	C 308	10.4	35.9	25	6	AR134674	AR134674 Sequence
236	10.6	36.6	26	6	AR171129	AR171129 Sequence	C 309	10.4	35.9	25	6	AX043151	AX043151 Sequence
237	10.6	36.6	26	6	AX068486	AX068486 Sequence	C 310	10.4	35.9	25	6	E35640	E35640 Murf. 2/200
238	10.6	36.6	26	6	AX068487	AX068487 Sequence	C 311	10.4	35.9	25	6	AR066703	AR066703 Sequence
239	10.6	36.6	26	6	A20867	A20867 Oligonucleo	C 312	10.4	35.9	27	6	AX117519	AX117519 Sequence
240	10.6	36.6	28	6	AR171134	AR171134 Sequence	C 313	10.4	35.9	27	6	AR080297	AR080297 Sequence
241	10.6	36.6	28	6	AX068492	AX068492 Sequence	C 314	10.4	35.9	28	6	AX117098	AX117098 Sequence
242	10.6	36.6	28	6	AX068492	AX068492 Sequence	C 315	10.4	35.9	29	6	AR080297	AR080297 Sequence
243	10.6	36.6	29	6	A78550	A78550 Sequence 7	C 316	10.4	35.9	29	6	AR080297	AR080297 Sequence
244	10.6	36.6	29	6	AR016291	AR016291 Sequence	C 317	10.4	35.9	30	6	AR053989	AR053989 Sequence
245	10.6	36.6	29	6	I07064	I07064 Sequence 7	C 318	10.4	35.9	30	6	AR135991	AR135991 Sequence
246	10.6	36.6	29	6	I60390	I60390 Sequence 7	C 319	10.4	35.9	30	6	AR138623	AR138623 Sequence
247	10.6	36.6	30	23	E10241	E10241 Oligonucleo	C 320	10.4	35.9	30	6	AX113443	AX113443 Sequence
248	10.6	36.6	31	6	AR087512	AR087512 Sequence	C 321	10.4	35.9	30	6	AX113578	AX113578 Sequence
249	10.6	36.6	31	6	AX033253	AX033253 Sequence	C 322	10.4	35.9	30	6	I22066	I22066 Sequence 3
250	10.6	36.6	32	6	AX030990	AX030990 Sequence	C 323	10.4	35.9	30	6	A00695	A00695 Artificial
251	10.6	36.6	32	6	AX107595	AX107595 Sequence	C 324	10.4	35.9	30	6	A00697	A00697 Artificial
252	10.6	36.6	34	6	AX083061	AX083061 Sequence	C 325	10.4	35.9	33	6	A00697	A00697 Artificial
253	10.6	36.6	36	6	AR075945	AR075945 Sequence	C 326	10.4	35.9	33	6	A22495	A22495 T-IF gene 5
254	10.6	36.6	37	6	E13173	E13173 PCR primer	C 327	10.4	35.9	33	6	AR054570	AR054570 Sequence
255	10.6	36.6	38	6	I06233	I06233 Sequence 5	C 328	10.4	35.9	33	6	AR054574	AR054574 Sequence
256	10.6	36.6	39	6	I81998	I81998 Sequence 37	C 329	10.4	35.9	33	6	I00406	I00406 Sequence 28
257	10.6	36.6	39	6	I91686	I91686 Sequence 36	C 330	10.4	35.9	33	6	I00409	I00409 Sequence 31
258	10.6	36.6	39	10	MMBAHRNA	X60884 M.musculus	C 331	10.4	35.9	34	10	AR357434	AR357434 Mus muscu
259	10.6	36.6	39	6	AX063573	AX063573 Sequence	C 332	10.4	35.9	35	6	A59049	A59049 Sequence 37
260	10.6	36.6	40	6	AX277042	AX277042 Sequence	C 333	10.4	35.9	35	6	AR175997	AR175997 Sequence
261	10.6	36.6	40	6	I09463	I09463 Sequence 1	C 334	10.4	35.9	35	6	I63326	I63326 Sequence 2
262	10.6	36.6	40	6	I09469	I09469 Sequence 7	C 335	10.4	35.9	35	6	A66385	A66385 Sequence 31
263	10.6	36.6	40	6	I09473	I09473 Sequence 11	C 336	10.4	35.9	37	6	A00725	A00725 Artificial
264	10.6	36.6	41	12	SYNHYGROB1	M31946 Synthetic h	C 337	10.4	35.9	37	6	A00725	A00725 Artificial
265	10.6	36.6	42	11	DOGCTPRAB	L77683 Carls fam11	C 338	10.4	35.9	38	6	I00983	I00983 Sequence 7
266	10.6	36.6	43	6	AR165375	AR165375 Sequence	C 339	10.4	35.9	38	6	BD004083	BD004083 Apoptosis
267	10.6	36.6	43	6	AR173096	AR173096 Sequence	C 340	10.4	35.9	40	6	AR176016	AR176016 Sequence
268	10.6	36.6	43	6	AX163117	AX163117 Sequence	C 341	10.4	35.9	40	6	I63345	I63345 Sequence 32
269	10.6	36.6	43	6	AX316318	AX316318 Sequence	C 342	10.4	35.9	44	6	A66386	A66386 Sequence 31
270	10.6	36.6	43	6	I26148	I26148 Sequence 8	C 343	10.4	35.9	45	6	A76101	A76101 Sequence 40
271	10.6	36.6	44	6	AR077448	AR077448 Sequence	C 344	10.4	35.9	45	5	XELRGT3B	XELRGT3B Sequence
272	10.6	36.6	46	6	AR003554	AR003554 Sequence	C 345	10.2	35.2	15	6	AR085136	AR085136 Sequence
273	10.6	36.6	47	6	AR011524	AR011524 Sequence	C 346	10.2	35.2	15	6	I77624	I77624 Sequence 33
274	10.6	36.6	47	6	AR011525	AR011525 Sequence	C 347	10.2	35.2	15	6	I77796	I77796 Sequence 50
275	10.6	36.6	47	6	AR077449	AR077449 Sequence	C 348	10.2	35.2	15	6	I77797	I77797 Sequence 50
276	10.6	36.6	47	6	AR110499	AR110499 Sequence	C 349	10.2	35.2	17	6	AX215157	AX215157 Sequence
277	10.6	36.6	47	6	AR110500	AR110500 Sequence	C 350	10.2	35.2	17	6	A41519	A41519 Sequence 12
278	10.6	36.6	47	6	AR137052	AR137052 Sequence	C 351	10.2	35.2	19	6	AX129570	AX129570 Sequence
279	10.6	36.6	47	6	AR137053	AR137053 Sequence	C 352	10.2	35.2	19	6	AX277050	AX277050 Sequence
280	10.6	36.6	47	6	AX194717	AX194717 Sequence	C 353	10.2	35.2	19	6	AX277060	AX277060 Sequence
281	10.6	36.6	47	6	AX194752	AX194752 Sequence	C 354	10.2	35.2	20	6	A78563	A78563 Sequence 20
282	10.6	36.6	47	6	AX194940	AX194940 Sequence	C 355	10.2	35.2	20	6	A78564	A78564 Sequence 21
283	10.6	36.6	47	6	AX234992	AX234992 Sequence	C 356	10.2	35.2	20	6	A98673	A98673 Sequence 8
284	10.6	36.6	47	6	I18162	I18162 Sequence 40	C 357	10.2	35.2	20	6	AR016304	AR016304 Sequence
285	10.6	36.6	48	6	I18163	I18163 Sequence 40	C 358	10.2	35.2	20	6	AR016305	AR016305 Sequence
286	10.6	36.6	48	14	HIVFLPBR4C	M92120 Human Immun	C 359	10.2	35.2	20	6	AR172935	AR172935 Sequence
287	10.6	36.6	50	6	AR077450	AR077450 Sequence	C 360	10.2	35.2	20	6	I60403	I60403 Sequence 20
288	10.4	35.9	15	6	I39454	I39454 Sequence 49	C 361	10.2	35.2	21	6	I60404	I60404 Sequence 21
289	10.4	35.9	16	6	A00723	A00723 Artificial	C 362	10.2	35.2	21	6	AX096535	AX096535 Sequence
290	10.4	35.9	18	6	AX026214	AX026214 Sequence	C 363	10.2	35.2	21	6	AX250525	AX250525 Sequence
291	10.4	35.9	18	9	S72956	S72956 estrogen re	C 364	10.2	35.2	21	6	E50674	E50674 Simple dete
292	10.4	35.9	20	6	AR117683	AR117683 Sequence	C 365	10.2	35.2	22	6	AR084023	AR084023 Sequence

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366	10.2	35.2	22	6	AR161997	AR161997 Sequence	439	10	34.5	20	6	AR095017	AR095017 Sequence
367	10.2	35.2	22	6	AR161999	AR161999 Sequence	440	10	34.5	20	6	AR126599	AR126599 Sequence
368	10.2	35.2	23	6	AR1517	AR1517 Sequence 44	c 441	10	34.5	20	6	AR173038	AR173038 Sequence
369	10.2	35.2	23	6	AR070168	AR070168 Sequence	442	10	34.5	20	6	AX049296	AX049296 Sequence
370	10.2	35.2	23	6	AX040598	AX040598 Sequence	443	10	34.5	20	6	AX056068	AX056068 Sequence
371	10.2	35.2	23	6	AX040598	AX040598 Sequence 10	444	10	34.5	20	6	AX088433	AX088433 Sequence
372	10.2	35.2	24	6	AX1517	AX1517 Sequence	445	10	34.5	20	6	AX108758	AX108758 Sequence
373	10.2	35.2	24	6	AR098011	AR098011 Sequence	c 446	10	34.5	20	6	IC2746	IC2746 Sequence 10
374	10.2	35.2	24	6	AR098033	AR098033 Sequence	447	10	34.5	20	6	184329	184329 Sequence 10
375	10.2	35.2	24	6	AR098041	AR098041 Sequence	c 448	10	34.5	20	12	AB069448	AB069448 Synthetic
376	10.2	35.2	24	6	AR098048	AR098048 Sequence	449	10	34.5	21	6	AX191776	AX191776 Sequence
377	10.2	35.2	24	6	AR171112	AR171112 Sequence	450	10	34.5	22	6	AR066925	AR066925 Sequence
378	10.2	35.2	24	6	AX068470	AX068470 Sequence	451	10	34.5	22	6	AR143675	AR143675 Sequence
379	10.2	35.2	24	6	BD011454	BD011454 Nucleic a	c 452	10	34.5	22	6	AR143701	AR143701 Sequence
380	10.2	35.2	24	6	BD011476	BD011476 Nucleic a	453	10	34.5	22	6	AR157249	AR157249 Sequence
381	10.2	35.2	24	6	BD011484	BD011484 Nucleic a	c 454	10	34.5	22	6	AR157275	AR157275 Sequence
382	10.2	35.2	24	6	BD011491	BD011491 Nucleic a	c 455	10	34.5	22	6	BD008729	BD008729 Novel pes
383	10.2	35.2	25	6	AX040597	AX040597 Sequence	c 456	10	34.5	22	6	BD008755	BD008755 Novel pes
384	10.2	35.2	25	6	AR183635	AR183635 Sequence	457	10	34.5	22	6	E59392	E59392 Method for
385	10.2	35.2	25	6	AX137641	AX137641 Sequence	458	10	34.5	22	6	AR165972	AR165972 Sequence
386	10.2	35.2	26	6	AX13990	AX13990 Nucleotide	459	10	34.5	23	6	AX104752	AX104752 Sequence
387	10.2	35.2	26	6	AX14001	AX14001 Nucleotide	c 460	10	34.5	23	6	AX104752	AX104752 Sequence
388	10.2	35.2	26	6	AX110704	AX110704 Sequence	461	10	34.5	23	6	E31905	E31905 Histidine k
389	10.2	35.2	26	6	AX137681	AX137681 Sequence	462	10	34.5	23	6	E60084	E60084 Endonucleas
390	10.2	35.2	27	6	AR9458	AR9458 Sequence 1	463	10	34.5	24	4	DOG2001P02	DOG2001P02
391	10.2	35.2	27	6	E63057	E63057 Na+/H+ anti	c 464	10	34.5	24	6	AR139369	AR139369 Sequence
392	10.2	35.2	28	6	AR07483	AR07483 Sequence	c 465	10	34.5	24	6	AR143977	AR143977 Sequence
393	10.2	35.2	28	6	AR165831	AR165831 Sequence	c 466	10	34.5	25	6	AR084685	AR084685 Sequence
394	10.2	35.2	29	6	AR169610	AR169610 Sequence	c 467	10	34.5	25	6	AR143663	AR143663 Sequence
395	10.2	35.2	30	6	AR028222	AR028222 Sequence	468	10	34.5	25	6	AR143691	AR143691 Sequence
396	10.2	35.2	30	6	AR138525	AR138525 Sequence	c 469	10	34.5	25	6	AR157237	AR157237 Sequence
397	10.2	35.2	30	6	AR157471	AR157471 Sequence	470	10	34.5	25	6	AR157265	AR157265 Sequence
398	10.2	35.2	30	6	AX281053	AX281053 Sequence	c 471	10	34.5	25	6	BD008717	BD008717 Novel pes
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401	10.2	35.2	30	6	AX282635	AX282635 Sequence	c 474	10	34.5	25	6	165326	165326 Sequence 5
402	10.2	35.2	30	6	AX288180	AX288180 Sequence	c 475	10	34.5	26	6	105141	105141 Sequence 5
403	10.2	35.2	31	6	AX115943	AX115943 Sequence	c 476	10	34.5	26	6	105319	105319 Sequence 2
404	10.2	35.2	31	6	AX1249324	AX1249324 Sequence	c 477	10	34.5	26	6	A69439	A69439 Sequence 71
405	10.2	35.2	31	6	AX155196	AX155196 Sequence	c 478	10	34.5	27	6	A72116	A72116 Sequence 71
406	10.2	35.2	32	6	AX183667	AX183667 Sequence	c 480	10	34.5	27	6	AR164827	AR164827 Sequence
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408	10.2	35.2	32	6	AR03342	AR03342 Sequence	c 482	10	34.5	27	6	AX226491	AX226491 Sequence
409	10.2	35.2	33	6	AR145735	AR145735 Sequence	c 483	10	34.5	27	6	BD003108	BD003108 Inhibitor
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414	10.2	35.2	34	6	AX226612	AX226612 Sequence	c 488	10	34.5	29	6	AR095256	AR095256 Sequence
415	10.2	35.2	35	6	AX085606	AX085606 Sequence	c 489	10	34.5	29	6	AR095258	AR095258 Sequence
416	10.2	35.2	35	6	AX044268	AX044268 Sequence	c 490	10	34.5	29	6	AR112603	AR112603 Sequence
417	10.2	35.2	40	6	IL5386	IL5386 Sequence 8	c 491	10	34.5	29	6	AR125223	AR125223 Sequence
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419	10.2	35.2	41	6	AR108511	AR108511 Sequence	c 493	10	34.5	30	6	AR3687	AR3687 Sequence
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421	10.2	35.2	41	6	IL6954	IL6954 Sequence 29	c 495	10	34.5	30	6	AR050260	AR050260 Sequence
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431	10.2	35.2	50	6	AF068856	AF068856 Mus sapi	c 505	10	34.5	32	6	AR156987	AR156987 Sequence
432	10.2	35.2	50	9	HSRPL1	HSRPL1	c 506	10	34.5	32	6	AR174613	AR174613 Sequence
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434	10.2	35.2	18	6	IS2008	IS2008 Sequence 6	c 508	10	34.5	32	6	AX146727	AX146727 Sequence
435	10.2	34.5	18	6	IS2008	IS2008 Sequence 6	c 509	10	34.5	33	6	AR031138	AR031138 Sequence
436	10.2	34.5	19	6	AX130144	AX130144 Sequence	c 510	10	34.5	33	6	AR050718	AR050718 Sequence
437	10.2	34.5	19	6	AX32763	AX32763 Synthetic c	c 511	10	34.5	33	6	AX114878	AX114878 Sequence
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A64069 Sequence 6
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AR167357 Sequence
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A30250 PS 24 const
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AR001613 Sequence
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AR132022 Sequence
c 974 9.6 33.1 36 6 AR132022 Sequence
AR170155 Sequence
c 975 9.6 33.1 36 6 AR170155 Sequence
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BD005318 Agent for
c 977 9.6 33.1 36 6 BD005318 Agent for
BD008615 Antifunga
c 978 9.6 33.1 36 6 BD008615 Antifunga
I77515 Sequence 22
c 979 9.6 33.1 36 6 I77515 Sequence 22
I78021 Sequence 72
c 980 9.6 33.1 36 6 I78021 Sequence 72
I78028 Sequence 73
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A28362 Hybridplasm
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AR046044 Sequence
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I53096 Sequence 83
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I84593 Sequence 2
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AX017754 Sequence
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ALIGNMENTS

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RESULT 1
A97472 A97472 19 bp DNA linear PAT 26-JAN-2000
LOCUS Sequence 28 from Patent WO9916780.
DEFINITION A97472
ACCESSION A97472
VERSION A97472.1 GI:6780818
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gala,J. and Vannuffel,P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
JOURNAL DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
Patent: WO 9916780-A 28 08-APR-1999;
GALA JEAN LOC (BE); UNIV LOUVAIN (BE)
FEATURES Location/Qualifiers

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 atgaattacacagagttaa 26
|||||
Db 1 ATGAATTTACAGACTTAA 19
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AX117627/c 27 bp DNA linear PAT 11-MAY-2001
LOCUS AX117627
DEFINITION Sequence 2750 from Patent WO0129262.
ACCESSION AX117627
VERSION AX117627.1 GI:14034578
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2750 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
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/note="primer"
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Db 19 TGAATTTACAGAG 6
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AR174977/c 33 bp DNA linear PAT 17-DEC-2001
LOCUS AR174977
DEFINITION Sequence 23 from patent US 6309644.
ACCESSION AR174977
VERSION AR174977.1 GI:17916276
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Chandrasekar,R. and Mehta,K.
TITLE Parasitic nematode transglutaminase proteins and uses thereof
JOURNAL Patent: US 6309644-A 23 30-OCT-2001;
Location/Qualifiers
FEATURES
source 1..33
/organism="unknown"
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ORIGIN
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 atgaattacaga 21
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 Db 33 ATGAATTACAGA 20

RESULT 4
 ARI74978 33 bp DNA linear PAT 17-DEC-2001
 LOCUS
 DEFINITION Sequence 24 from patent US 6309644.
 ARI74978
 VERSION ARI74978.1 GI:17916277
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
 AUTHORS Chandrasekar, R. and Mehta, K.
 TITLE Parasitic nematode transglutaminase proteins and uses thereof
 JOURNAL Patent: US 6309644-A 24 30-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unknown"

BASE COUNT 11 a 7 c 9 g 6 t
 ORIGIN

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QY 8 atgaattacaga 21
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 Db 13 ATGAATTACAGA 26

RESULT 5
 ARI74999 45 bp DNA linear PAT 17-DEC-2001
 LOCUS
 DEFINITION Sequence 51 from patent US 6309644.
 ARI74999
 VERSION ARI74999.1 GI:17916298
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
 AUTHORS Chandrasekar, R. and Mehta, K.
 TITLE Parasitic nematode transglutaminase proteins and uses thereof
 JOURNAL Patent: US 6309644-A 51 30-OCT-2001;
 FEATURES Location/Qualifiers
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BASE COUNT 14 a 5 c 16 g 10 t
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QY 8 atgaattacaga 21
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 Db 13 ATGAATTACAGA 26

RESULT 6
 ARI75000 45 bp DNA linear PAT 17-DEC-2001
 LOCUS
 DEFINITION Sequence 53 from patent US 6309644.
 ARI75000
 VERSION ARI75000.1 GI:17916299
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 45)
 AUTHORS Chandrasekar, R. and Mehta, K.
 TITLE Parasitic nematode transglutaminase proteins and uses thereof
 JOURNAL Patent: US 6309644-A 53 30-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..45
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BASE COUNT 10 a 16 c 5 g 14 t
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 Db 33 ATGAATTACAGA 20

RESULT 7
 AX130141 19 bp DNA linear PAT 15-MAY-2001
 LOCUS
 DEFINITION Sequence 1359 from Patent WO0130362.
 AX130141
 VERSION AX130141.1 GI:14136446
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 AUTHORS Robbins, J.M. and Tritz, R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
 JOURNAL Patent: WO 0130362-A 1359 03-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /note="cdk-we-hu ribozyme binding site"

BASE COUNT 7 a 4 c 3 g 5 t
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 aattacagagt 24
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 Db 7 AATTACAGGTT 19

RESULT 8
 AX130142 19 bp DNA linear PAT 15-MAY-2001
 LOCUS
 DEFINITION Sequence 1360 from Patent WO0130362.
 AX130142
 VERSION AX130142.1 GI:14136447
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 AUTHORS Robbins, J.M. and Tritz, R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases

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JOURNAL Patent: WO 0130362-A 1360 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. 19
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/note="Cdk-we-hu ribozyme binding site"
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 aattacaggtt 24
Db 6 AATTACAGGTT 18

RESULT 9
LOCUS AX130143 19 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 1361 from Patent WO0130362.
ACCESSION AX130143
VERSION AX130143.1 GI:14136448
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Robbins,J.M. and Tritz,R.
JOURNAL Ribozyme therapy for the treatment of proliferative skin and eye diseases
Patent: WO 0130362-A 1361 03-MAY-2001;
IMMUSOL, INC. (US)

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/note="Cdk-we-hu ribozyme binding site"
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 aattacaggtt 24
Db 5 AATTACAGGTT 17

RESULT 10
LOCUS AR043211/c 24 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 95 from patent US 5814453.
ACCESSION AR043211
VERSION AR043211.1 GI:5964219
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Beck,J.Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 95 29-SEP-1998;
FEATURES Location/Qualifiers
source 1. 24
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BASE COUNT 7 a 4 c 2 g 11 t

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Best Local Similarity 87.5%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 11 aaattacagaggttaa 26
Db 6 AAAATTACAGAGTTAA 21

ORIGIN

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Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 11 aaattacagaggttaa 26
Db 17 AAATTACAGAGTTTA 2

RESULT 11
LOCUS AR050529 24 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5827695.
ACCESSION AR050529
VERSION AR050529.1 GI:5973254
KEYWORDS Unknown.
SOURCE Unknown.

ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Beck,J.Joseph.
TITLE Detection of wheat fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5827695-A 15 27-OCT-1998;
FEATURES Location/Qualifiers
source 1. 24
/organism="unknown"
BASE COUNT 7 a 4 c 2 g 11 t
ORIGIN

Query Match 44.1%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 11 aaattacagaggttaa 26
Db 17 AAATTACAGAGTTTA 2

RESULT 12
LOCUS AR166684 28 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 34 from patent US 6281346.
ACCESSION AR166684
VERSION AR166684.1 GI:16242098
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Hess,J.W., Caskey,C.Thomas., Liu,Q. and Phillips,M.Sea.
TITLE Rat ob-receptors and nucleotides encoding them
JOURNAL Patent: US 6281346-A 34 28-AUG-2001;
FEATURES Location/Qualifiers
source 1. 28
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 11 aaattacagaggttaa 26
Db 6 AAAATTACAGAGTTAA 21

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RESULT 13
LOCUS A12544 35 bp DNA linear PAT 07-DEC-1993
DEFINITION polypeptide actin.
ACCESSION A12544
VERSION A12544.1 GI:491391
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 35)
ARTHORS
TITLE ENHANCED SECRETION OF HETEROLOGOUS PROTEINS BY HOSTS USING
SUBSTITUTED PROMOTERS
JOURNAL Patent: WO 8703300-A 15 04-JUN-1987;
FEATURES
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DB 7 AAATTACTGAATTAA 22

RESULT 14
LOCUS A97446 35 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 2 from Patent WO916780.
ACCESSION A97446
VERSION A97446.1 GI:6780792
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 35)
ARTHORS Gala, J. and Vannuffel, P.
TITLE GENERIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 916780-A 2 08-APR-1999;
FEATURES
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Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 atgaattacagagtaa 26
||||| ||||| |||
DB 4 ATGAATTACNAATTNA 22

RESULT 15
LOCUS A12546 39 bp DNA linear PAT 07-DEC-1993
DEFINITION polypeptide pex-8.
ACCESSION A12546
VERSION A12546.1 GI:491393
KEYWORDS
SOURCE synthetic construct.

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ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 39)
ARTHORS
TITLE ENHANCED SECRETION OF HETEROLOGOUS PROTEINS BY HOSTS USING
SUBSTITUTED PROMOTERS
JOURNAL Patent: WO 8703300-A 17 04-JUN-1987;
FEATURES
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Query Match 44.1%; Score 12.8; DB 6; Length 39;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 aaattacagagtaa 26
||||| ||||| |||
DB 7 AAATTACTGAATTAA 22

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OW nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:09:49 ; Search time 286.45 Seconds

(Without alignments)
173.819 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1300_1328
Sequence: 1 nnnnnnataattacagagtaann 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1042728

Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 1000 summaries

Database : N_Geneseq_032802.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	19	65.5	19 20 AA337776	Staphylococcus sp.
2	18	62.1	29 20 AA337792	Staphylococcus sp.
3	14	48.3	27 22 AA339954	SNP specific lower
4	14	48.3	33 19 AA330329	Dicrofilaria immiti
5	14	48.3	33 19 AA330330	Dicrofilaria immiti
6	14	48.3	33 24 AA67837	D. immitis transgl
7	14	48.3	33 24 AA67838	D. immitis transgl
8	14	48.3	45 24 AA67859	D. immitis transgl
9	14	48.3	45 24 AA67860	Complementary stra

10	13.4	46.2	15	22	AA537714	IGF-1 oligonucleot
11	13	44.8	19	21	AA83773	cdk-we-hu ribozyme
12	13	44.8	19	21	AA83774	cdk-we-hu ribozyme
13	13	44.8	19	21	AA83775	cdk-we-hu ribozyme
14	13	44.8	19	22	AA58935	cdk-we-hu ribozyme
15	13	44.8	19	22	AA58936	cdk-we-hu ribozyme
16	13	44.8	19	22	AA58937	cdk-we-hu ribozyme
17	12.8	44.1	24	19	AA59018	Internal transcrib
18	12.8	44.1	24	19	AA59018	Internal transcrib
19	12.8	44.1	24	19	AA59018	Internal transcrib
20	12.8	44.1	24	19	AA59018	Internal transcrib
21	12.6	43.4	22	19	AA59018	Internal transcrib
22	12.6	43.4	22	19	AA59018	Internal transcrib
23	12.6	43.4	22	19	AA59018	Internal transcrib
24	12.6	43.4	22	19	AA59018	Internal transcrib
25	12.6	43.4	22	19	AA59018	Internal transcrib
26	12.6	43.4	22	19	AA59018	Internal transcrib
27	12.6	43.4	22	19	AA59018	Internal transcrib
28	12.6	43.4	22	19	AA59018	Internal transcrib
29	12.6	43.4	22	19	AA59018	Internal transcrib
30	12.6	43.4	22	19	AA59018	Internal transcrib
31	12.6	43.4	22	19	AA59018	Internal transcrib
32	12.6	43.4	22	19	AA59018	Internal transcrib
33	12.6	43.4	22	19	AA59018	Internal transcrib
34	12.6	43.4	22	19	AA59018	Internal transcrib
35	12.6	43.4	22	19	AA59018	Internal transcrib
36	12.6	43.4	22	19	AA59018	Internal transcrib
37	12.6	43.4	22	19	AA59018	Internal transcrib
38	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
39	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
40	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
41	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
42	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
43	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
44	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
45	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
46	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
47	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
48	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
49	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
50	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
51	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
52	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
53	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
54	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
55	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
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58	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
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64	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
65	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
66	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
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75	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
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78	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
79	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
80	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
81	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot
82	12.4	42.8	15	22	AA537715	IGF-1 oligonucleot

Fibrinogen G-gamma

c 83	11.8	40.7	30	17	AAT28511	S. epidermidis det	156	11.4	39.3	22	18	AAT47392	Primer #18 for cys
c 84	11.8	40.7	35	22	ABA76971	Staphylococcus epi	157	11.4	39.3	23	20	AAZ28426	Minus strand PCR p
c 85	11.8	40.7	35	13	AAQ33431	P(-1) stem-loop of	c 158	11.4	39.3	26	22	AAH01483	dhfrv resistance g
c 86	11.8	40.7	35	14	AAQ51734	Modified P(-1) ste	159	11.4	39.3	28	16	AAQ88386	CFTR amplification
c 87	11.8	40.7	45	22	AAH50315	Bacterial 235/58 R	160	11.4	39.3	28	21	AAA06076	CFTR gene analysis
c 88	11.8	40.7	45	22	AAH50315	Oligonucleotide us	c 161	11.4	39.3	30	22	AAQ53230	Human Oestrogen re
c 89	11.8	40.7	45	22	AAH5449	Oligonucleotide us	c 162	11.4	39.3	32	16	AAQ95024	Template oligo CF1
c 90	11.8	40.7	45	22	AAH5450	Oligonucleotide us	163	11.4	39.3	33	22	AAH19116	Amplification comm
c 91	11.8	40.7	45	22	AAH5198	Human retrovirus D	164	11.4	39.3	34	16	AAH19116	Fragment of cDNA e
c 92	11.8	40.7	45	22	AAH52216	Human retrovirus D	165	11.4	39.3	34	16	AAH19116	Human Wp1 hybrid
c 93	11.8	40.7	45	22	AAH52216	Human retrovirus D	166	11.4	39.3	34	16	AAH19116	Intron-exon juncti
c 94	11.8	40.7	45	22	AAH52216	Oligonucleotide TA	167	11.4	39.3	36	18	AAH19116	Vaccinia virus A8L
c 95	11.8	40.7	45	22	AAH52216	Oligonucleotide TA	c 168	11.4	39.3	36	18	AAH19116	CFTR gene exon 11
c 96	11.8	40.7	47	21	AAH52216	Human map-related	169	11.4	39.3	44	16	AAH19116	CFTR gene exon 11
c 97	11.8	40.7	47	21	AAH52216	Human map-related	170	11.4	39.3	44	16	AAH19116	CFTR gene analysis
c 98	11.8	40.7	47	21	AAH52216	Human map-related	171	11.4	39.3	44	21	AAH19116	CFTR gene analysis
c 99	11.8	40.7	47	21	AAH52216	Human map-related	172	11.4	39.3	44	21	AAH19116	Human map-related
c 100	11.8	40.7	50	22	AAH51066	CNS disorder-relat	c 173	11.4	39.3	50	20	AAH51066	Synthetic plasmid
c 101	11.8	40.7	50	22	AAH51066	Oligonucleotide SE	174	11.4	39.3	50	20	AAH51066	Synthetic plasmid
c 102	11.8	40.7	50	22	AAH51066	Human ngPCR56 PCR	c 175	11.4	39.3	50	22	AAH51066	Human SNP oligonuc
c 103	11.8	40.7	50	22	AAH51066	Nucleotide sequenc	c 176	11.2	38.6	16	19	AAV48823	Erbs-2 gene antisense
c 104	11.6	40.0	19	21	AAH48521	Cyclin E ribozyme	177	11.2	38.6	17	19	AAV17071	Interferon (IFN)-b
c 105	11.6	40.0	19	21	AAH48521	Cyclin E ribozyme	178	11.2	38.6	17	23	ABK00600	Human NCO Zinzhyme
c 106	11.6	40.0	20	22	AAH59683	Human DAD-1 gene a	179	11.2	38.6	17	23	ABK00600	Human NCO Zinzhyme
c 107	11.6	40.0	21	21	AAH59683	Mammalian interleu	c 180	11.2	38.6	18	20	AAH59683	Primer for nucleic
c 108	11.6	40.0	24	24	AAH59683	Ribosome L39 prote	181	11.2	38.6	18	21	AAH59683	Human G-alpha-16 a
c 109	11.6	40.0	24	24	AAH59683	Human mper3-23 PCR	c 182	11.2	38.6	19	21	AAH59683	Cyclin E ribozyme
c 110	11.6	40.0	28	16	AAH59683	-271 to -244 of ri	c 183	11.2	38.6	19	22	AAH59683	Cyclin E ribozyme
c 111	11.6	40.0	28	16	AAH59683	Neurofibromatosis	184	11.2	38.6	20	21	AAH59683	GUS gene oligonuc
c 112	11.6	40.0	29	14	AAH59683	Sequence of 3SR pr	185	11.2	38.6	20	21	AAH59683	Staphylococcus aur
c 113	11.6	40.0	29	14	AAH59683	KDEL-deleted heat	c 186	11.2	38.6	22	18	AAH59683	PCR primer used to
c 114	11.6	40.0	29	14	AAH59683	Human MPL3 PCR pri	c 187	11.2	38.6	22	22	AAH59683	Human DP2.5 APC pr
c 115	11.6	40.0	32	19	AAH59683	Human MPL3 PCR pri	c 188	11.2	38.6	23	19	AAH59683	MBR primer for Maj
c 116	11.6	40.0	32	19	AAH59683	Flt-3 ligand prime	c 189	11.2	38.6	23	20	AAH59683	Ze mays genome re
c 117	11.6	40.0	32	20	AAH59683	Primer HIND165 for	c 190	11.2	38.6	24	13	AAH59683	Hamster BHKsfz CDN
c 118	11.6	40.0	32	21	AAH59683	Human MTP promoter	c 191	11.2	38.6	24	19	AAH59683	Dog genomic marker
c 119	11.6	40.0	33	21	AAH59683	Primer for interfe	c 192	11.2	38.6	25	19	AAH59683	SNP specific SNPE
c 120	11.6	40.0	33	20	AAH59683	PCR primer for int	c 193	11.2	38.6	25	22	AAH59683	SNP specific SNPE
c 121	11.6	40.0	33	22	AAH59683	Human quinoprotein	c 194	11.2	38.6	25	22	AAH59683	Human IL-1ra gamma
c 122	11.6	40.0	34	21	AAH59683	Complement C3-degr	c 195	11.2	38.6	25	22	AAH59683	Human biallelic po
c 123	11.6	40.0	35	19	AAH59683	Primer OVT330 used	c 196	11.2	38.6	26	25	AAH59683	Human progesterone
c 124	11.6	40.0	35	20	AAH59683	PCR primer OVT 330	c 197	11.2	38.6	27	22	AAH59683	Primer for human p
c 125	11.6	40.0	35	22	AAH59683	3' PCR primer OT-1	c 198	11.2	38.6	28	18	AAH59683	Human biallelic po
c 126	11.6	40.0	36	21	AAH59683	C. tetani tetanus	c 199	11.2	38.6	28	18	AAH59683	Human biallelic po
c 127	11.6	40.0	36	21	AAH59683	Primer for interfe	c 200	11.2	38.6	28	19	AAH59683	Breast cancer spec
c 128	11.6	40.0	37	19	AAH59683	Encodes immunogeni	c 201	11.2	38.6	30	14	AAH59683	Yeast optimised GF
c 129	11.6	40.0	39	14	AAH59683	-230 to -192 of ri	c 202	11.2	38.6	30	14	AAH59683	Nucleotide fragmen
c 130	11.6	40.0	39	16	AAH59683	c-jun RNA substrat	c 203	11.2	38.6	31	19	AAH59683	Nucleotide fragmen
c 131	11.6	40.0	40	18	AAH59683	Human derived cyto	c 204	11.2	38.6	31	19	AAH59683	Human genomic DNA
c 132	11.6	40.0	40	20	AAH59683	Human quinoprotein	c 205	11.2	38.6	31	19	AAH59683	Human genomic DNA
c 133	11.6	40.0	41	22	AAH59683	Human GARA protein	c 206	11.2	38.6	31	20	AAH59683	Pseudo-LoxP site B
c 134	11.6	40.0	41	24	AAH59683	Human SNP oligonuc	c 207	11.2	38.6	34	21	AAH59683	Dirotifilaria immiti
c 135	11.6	40.0	45	22	AAH59683	PCR primer 141223,	c 208	11.2	38.6	39	16	AAH59683	Probe no.3 for the
c 136	11.6	40.0	45	22	AAH59683	Nucleotide sequenc	c 209	11.2	38.6	39	16	AAH59683	HPV type 18 exon-s
c 137	11.6	40.0	47	19	AAH59683	Human map-related	c 210	11.2	38.6	40	9	AAH59683	Maize polymorphic
c 138	11.6	40.0	47	21	AAH59683	Human map-related	c 211	11.2	38.6	40	18	AAH59683	Human cerebral pro
c 139	11.6	40.0	47	21	AAH59683	Human map-related	c 212	11.2	38.6	40	19	AAH59683	Cystic fibrosis tr
c 140	11.6	40.0	50	22	AAH59683	Human SNP oligonuc	c 213	11.2	38.6	40	20	AAH59683	Legionella RNA sp
c 141	11.6	40.0	50	22	AAH59683	IGF-I oligonucleot	c 214	11.2	38.6	40	20	AAH59683	PCR primer for pep
c 142	11.4	39.3	15	22	AAH59683	Probe based on N-t	c 215	11.2	38.6	40	22	AAH59683	Probe used to date
c 143	11.4	39.3	21	13	AAH59683	Toxin gene 33f2 pr	c 216	11.2	38.6	41	19	AAH59683	Hirudin acidic dom
c 144	11.4	39.3	21	13	AAH59683	Ant-active toxin g	c 217	11.2	38.6	42	21	AAH59683	Probe used to date
c 145	11.4	39.3	21	13	AAH59683	Reverse PCR primer	c 218	11.2	38.6	44	18	AAH59683	Human CFTR gene ch
c 146	11.4	39.3	21	16	AAH59683	B.t. toxin probe 3	c 219	11.2	38.6	44	21	AAH59683	Human CFTR gene mu
c 147	11.4	39.3	21	16	AAH59683	Cysteine protease	c 220	11.2	38.6	44	22	AAH59683	Human CFTR gene ch
c 148	11.4	39.3	21	18	AAH59683	Bacillus thuringie	c 221	11.2	38.6	46	22	AAH59683	Human H4 histone g
c 149	11.4	39.3	21	18	AAH59683	Probe 63B-A/33F2B	c 222	11.2	38.6	46	22	AAH59683	Human H4 histone g
c 150	11.4	39.3	21	19	AAH59683	B.t. toxin gene pr	c 223	11.2	38.6	47	15	AAH59683	Test sequence from
c 151	11.4	39.3	21	19	AAH59683	Probe 33F2B used t	c 224	11.2	38.6	47	18	AAH59683	Human map-related
c 152	11.4	39.3	21	22	AAH59683	Probe 33F2B, Baci	c 225	11.2	38.6	47	20	AAH59683	
c 153	11.4	39.3	21	22	AAH59683	Bacillus thuringie	c 226	11.2	38.6	47	20	AAH59683	
c 154	11.4	39.3	21	24	AAH59683	HIV gag-env chimera	c 227	11.2	38.6	47	21	AAH59683	
c 155	11.4	39.3	22	15	AAH59683		c 228	11.2	38.6	47	21	AAH59683	

C 229	11.2	38.6	47	21	AAZ69174	Human map-related	C 302	10.8	37.2	20	22	AAZ69174	Human catenin-bind
C 230	11.2	38.6	50	22	AAZ69170	Human SNP oligonuc	C 303	10.8	37.2	21	18	AAZ69170	CFTR binding site
C 231	11.2	38.6	50	22	AAZ69170	Human SNP oligonuc	C 304	10.8	37.2	21	21	AAZ69170	Human biallelic ma
C 232	11.2	38.6	50	22	AAZ69170	Human silent SNP c	C 305	10.8	37.2	21	22	AAZ69170	Human gene single
C 233	11.2	38.6	50	23	AAZ69170	Human silent nonco	C 306	10.8	37.2	24	13	AAZ69170	Sequence upstream
C 234	11.2	38.6	15	22	AAZ69170	IGF-1 oligonucleot	C 307	10.8	37.2	24	16	AAZ69170	Human IL1B 2q3-q21
C 235	11.2	38.6	15	22	AAZ69170	Human EGF-R target	C 308	10.8	37.2	24	16	AAZ69170	Human IL1B 2q3-q21
C 236	11.2	38.6	17	19	AAZ69170	Human EGF-R target	C 309	10.8	37.2	24	21	AAZ69170	Forward primer FIV
C 237	11.2	38.6	17	19	AAZ69170	Human EGF-R target	C 310	10.8	37.2	24	21	AAZ69170	Short tandem repea
C 238	11.2	38.6	20	19	AAZ69170	Insecticidal toxin	C 311	10.8	37.2	25	13	AAZ69170	Upstream PCR prime
C 239	11.2	38.6	21	21	AAZ69170	Human biallelic ma	C 312	10.8	37.2	25	19	AAZ69170	Primer used to det
C 240	11.2	38.6	22	21	AAZ69170	Forward primer #12	C 313	10.8	37.2	25	21	AAZ69170	Alzheimer's diseas
C 241	11.2	38.6	22	21	AAZ69170	Human myosin heavy	C 314	10.8	37.2	25	22	AAZ69170	Soybean 318013 reg
C 242	11.2	38.6	24	22	AAZ69170	TNFR/NGFR protein	C 315	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 243	11.2	38.6	25	20	AAZ69170	PCR primer for hum	C 316	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 244	11.2	38.6	25	20	AAZ69170	Bacteriophage 96 O	C 317	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 245	11.2	38.6	25	21	AAZ69170	Bacteriophage 96 O	C 318	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 246	11.2	38.6	25	21	AAZ69170	Human fli1 VEGF re	C 319	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 247	11.2	38.6	27	18	AAZ69170	PCR primer for cel	C 320	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 248	11.2	38.6	27	19	AAZ69170	GTT-IV CDNA contai	C 321	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 249	11.2	38.6	27	19	AAZ69170	Human biallelic po	C 322	10.8	37.2	26	18	AAZ69170	Human Papillomavir
C 250	11.2	38.6	28	19	AAZ69170	Oligonucleotide pr	C 323	10.8	37.2	26	20	AAZ69170	Human Papillomavir
C 251	11.2	38.6	29	20	AAZ69170	Human secreted pro	C 324	10.8	37.2	27	17	AAZ69170	Human Papillomavir
C 252	11.2	38.6	29	20	AAZ69170	Biotinylated oligo	C 325	10.8	37.2	27	17	AAZ69170	Single nucleotide
C 253	11.2	38.6	30	21	AAZ69170	552 top primer to	C 326	10.8	37.2	27	21	AAZ69170	Human ST drug-met
C 254	11.2	38.6	31	19	AAZ69170	Nucleotide fragmen	C 327	10.8	37.2	27	22	AAZ69170	Tobacco mosaic vir
C 255	11.2	38.6	31	19	AAZ69170	Human genomic DNA	C 328	10.8	37.2	27	23	AAZ69170	PCR primer for fun
C 256	11.2	38.6	31	21	AAZ69170	NPS-326 primer. S	C 329	10.8	37.2	28	19	AAZ69170	Primer C7-alpha-H
C 257	11.2	38.6	32	14	AAZ69170	Human uterine glob	C 330	10.8	37.2	30	15	AAZ69170	L. mesenteroides a
C 258	11.2	38.6	33	24	AAZ69170	Neisseria meningit	C 331	10.8	37.2	30	21	AAZ69170	First round sense
C 259	11.2	38.6	34	22	AAZ69170	DNA ligase 10 PCR	C 332	10.8	37.2	30	21	AAZ69170	Lactuce Infectious
C 260	11.2	38.6	34	22	AAZ69170	Primer P3 for E. c	C 333	10.8	37.2	31	16	AAZ69170	Human CTR gene as
C 261	11.2	38.6	36	21	AAZ69170	PCR primer W57 use	C 334	10.8	37.2	31	16	AAZ69170	Primer for interfe
C 262	11.2	38.6	36	21	AAZ69170	PCR primer 2 used	C 335	10.8	37.2	32	22	AAZ69170	Human RNA uncollin
C 263	11.2	38.6	37	16	AAZ69170	Human gene signatu	C 336	10.8	37.2	33	19	AAZ69170	DNA footprinting p
C 264	11.2	38.6	37	16	AAZ69170	11L promoter-HTLV	C 337	10.8	37.2	33	22	AAZ69170	Primer LMN226 for
C 265	11.2	38.6	38	17	AAZ69170	M11-11/III synthe	C 338	10.8	37.2	34	18	AAZ69170	Intinon-exon juncti
C 266	11.2	38.6	38	18	AAZ69170	Staphylococcus aur	C 339	10.8	37.2	36	15	AAZ69170	Oligonucleotide C-
C 267	11.2	38.6	38	24	AAZ69170	Human truncated AP	C 340	10.8	37.2	36	18	AAZ69170	B. subtilis jumaz1
C 268	11.2	38.6	39	21	AAZ69170	Human p21-like G p	C 341	10.8	37.2	37	21	AAZ69170	Heat shock protein
C 269	11.2	38.6	39	24	AAZ69170	Optum poppy berber	C 342	10.8	37.2	38	16	AAZ69170	MalE-Hsp fusion pr
C 270	11.2	38.6	40	19	AAZ69170	Brassica sp. polyu	C 343	10.8	37.2	38	17	AAZ69170	Neisseria species
C 271	11.2	38.6	41	19	AAZ69170	Haemophilus influe	C 344	10.8	37.2	38	21	AAZ69170	E. coli xylB PCR p
C 272	11.2	38.6	41	21	AAZ69170	Cerebral specific	C 345	10.8	37.2	38	24	AAZ69170	Sequence upstream
C 273	11.2	38.6	41	24	AAZ69170	Plasmid pCIVYV con	C 346	10.8	37.2	39	21	AAZ69170	Human map-related
C 274	11.2	38.6	44	21	AAZ69170	Single base extens	C 347	10.8	37.2	46	13	AAZ69170	Human map-related
C 275	11.2	38.6	45	21	AAZ69170	DNA encoding class	C 348	10.8	37.2	47	21	AAZ69170	Human map-related
C 276	11.2	38.6	45	22	AAZ69170	S. cerevisiae YKR0	C 349	10.8	37.2	47	21	AAZ69170	Human map-related
C 277	11.2	38.6	45	22	AAZ69170	S. cerevisiae YOL0	C 350	10.8	37.2	47	21	AAZ69170	Human map-related
C 278	11.2	38.6	45	22	AAZ69170	PCR primer #55 use	C 351	10.8	37.2	47	21	AAZ69170	CFTR binding site
C 279	11.2	38.6	46	14	AAZ69170	Human map-related	C 352	10.8	37.2	49	18	AAZ69170	Analyte capture pr
C 280	11.2	38.6	47	21	AAZ69170	Human map-related	C 353	10.8	37.2	50	12	AAZ69170	Single stranded DN
C 281	11.2	38.6	47	21	AAZ69170	Human map-related	C 354	10.8	37.2	50	17	AAZ69170	HIV analyte captur
C 282	11.2	38.6	47	21	AAZ69170	Human map-related	C 355	10.8	37.2	50	20	AAZ69170	Enzymatic DNA frag
C 283	11.2	38.6	47	21	AAZ69170	Human map-related	C 356	10.8	37.2	50	22	AAZ69170	Human SNP oligonuc
C 284	11.2	38.6	47	21	AAZ69170	Human map-related	C 357	10.8	37.2	50	22	AAZ69170	Human SNP oligonuc
C 285	11.2	38.6	47	21	AAZ69170	Human map-related	C 358	10.8	37.2	50	22	AAZ69170	Mouse fli-1 VEGF r
C 286	11.2	38.6	47	21	AAZ69170	Human map-related	C 359	10.6	36.6	17	18	AAZ69170	Novel strand displ
C 287	11.2	38.6	50	14	AAZ69170	BoxC consensus seq	C 360	10.6	36.6	18	21	AAZ69170	Novel strand displ
C 288	10.8	37.2	50	19	AAZ69170	EtB-2 gene antisec	C 361	10.6	36.6	18	21	AAZ69170	Novel strand displ
C 289	10.8	37.2	51	15	AAZ69170	EtB-2 gene antisec	C 362	10.6	36.6	18	21	AAZ69170	Allele-specific st
C 290	10.8	37.2	16	18	AAZ69170	Probe 74m10 for dr	C 363	10.6	36.6	18	21	AAZ69170	Bacterial 16S RNA
C 291	10.8	37.2	16	18	AAZ69170	Probe 74m11 for dr	C 364	10.6	36.6	18	22	AAZ69170	Novel strand displ
C 292	10.8	37.2	17	17	AAZ69170	Human c-myc hamme	C 365	10.6	36.6	18	22	AAZ69170	Novel strand displ
C 293	10.8	37.2	17	17	AAZ69170	Human c-myc hamme	C 366	10.6	36.6	19	21	AAZ69170	Cdk-ve-hu ribozyme
C 294	10.8	37.2	17	17	AAZ69170	Human c-myc hamme	C 367	10.6	36.6	19	21	AAZ69170	Cyclin G1 ribozyme
C 295	10.8	37.2	17	18	AAZ69170	Probe 74m12 for dr	C 368	10.6	36.6	19	22	AAZ69170	Cdk-ve-hu ribozyme
C 296	10.8	37.2	17	21	AAZ69170	Oestrogen receptor	C 369	10.6	36.6	19	22	AAZ69170	Cyclin G1 ribozyme
C 297	10.8	37.2	18	21	AAZ69170	Human biallelic ma	C 370	10.6	36.6	20	20	AAZ69170	PCR primer used to
C 298	10.8	37.2	19	22	AAZ69170	Human inflammatory	C 371	10.6	36.6	20	20	AAZ69170	PCR primer used to
C 299	10.8	37.2	20	17	AAZ69170	Probe for enteroba	C 372	10.6	36.6	20	20	AAZ69170	Human MDKX antisen
C 300	10.8	37.2	20	21	AAZ69170	Human biallelic ma	C 373	10.6	36.6	20	21	AAZ69170	Human cot oncogene
C 301	10.8	37.2	20	22	AAZ69170	Human ANC_2H01 cDN	C 374	10.6	36.6	20	22	AAZ69170	

375	10.6	36.6	20	22	AAF82210	Melon ethylene rec	448	10.6	36.6	15	AAQ66291	CryIA(a) PCR prime
376	10.6	36.6	21	17	AA704054	Corynebacterium sp	449	10.6	36.6	17	AA79477	Bacillus thuringie
377	10.6	36.6	21	21	AAZ70479	Human biallelic ma	450	10.6	36.6	19	AAV39142	Primer 11 for age1
378	10.6	36.6	21	21	AAZ73869	Human biallelic ma	451	10.6	36.6	19	AAV39142	PCR primer used to
379	10.6	36.6	21	21	AAZ73869	RT-PCR forward pri	452	10.6	36.6	22	AAZ20083	B. thuringiensis i
380	10.6	36.6	21	22	AAZ09158	Human stem cell fa	453	10.6	36.6	24	ABK16688	Leptin receptor (L
381	10.6	36.6	21	22	AAZ11047	Bacterial 16S RNA	454	10.6	36.6	24	ABK16688	Leptin receptor (L
382	10.6	36.6	21	22	AAZ11053	Human stem cell fa	455	10.6	36.6	24	ABK16688	Leptin receptor (L
383	10.6	36.6	21	22	AAZ11053	Human stem cell fa	456	10.6	36.6	24	ABK16688	Leptin receptor (L
384	10.6	36.6	21	22	AAZ11053	Human stem cell fa	457	10.6	36.6	24	ABK16688	Leptin receptor (L
385	10.6	36.6	21	22	AAZ11053	Human stem cell fa	458	10.6	36.6	24	ABK16688	Leptin receptor (L
386	10.6	36.6	21	22	AAZ11053	Human stem cell fa	459	10.6	36.6	24	ABK16688	Leptin receptor (L
387	10.6	36.6	21	22	AAZ11053	Human stem cell fa	460	10.6	36.6	24	ABK16688	Leptin receptor (L
388	10.6	36.6	21	22	AAZ11053	Human stem cell fa	461	10.6	36.6	24	ABK16688	Leptin receptor (L
389	10.6	36.6	21	22	AAZ11053	Human stem cell fa	462	10.6	36.6	24	ABK16688	Leptin receptor (L
390	10.6	36.6	21	22	AAZ11053	Human stem cell fa	463	10.6	36.6	24	ABK16688	Leptin receptor (L
391	10.6	36.6	21	22	AAZ11053	Human stem cell fa	464	10.6	36.6	24	ABK16688	Leptin receptor (L
392	10.6	36.6	21	22	AAZ11053	Human stem cell fa	465	10.6	36.6	24	ABK16688	Leptin receptor (L
393	10.6	36.6	21	22	AAZ11053	Human stem cell fa	466	10.6	36.6	24	ABK16688	Leptin receptor (L
394	10.6	36.6	21	22	AAZ11053	Human stem cell fa	467	10.6	36.6	24	ABK16688	Leptin receptor (L
395	10.6	36.6	21	22	AAZ11053	Human stem cell fa	468	10.6	36.6	24	ABK16688	Leptin receptor (L
396	10.6	36.6	21	22	AAZ11053	Human stem cell fa	469	10.6	36.6	24	ABK16688	Leptin receptor (L
397	10.6	36.6	21	22	AAZ11053	Human stem cell fa	470	10.6	36.6	24	ABK16688	Leptin receptor (L
398	10.6	36.6	21	22	AAZ11053	Human stem cell fa	471	10.6	36.6	24	ABK16688	Leptin receptor (L
399	10.6	36.6	21	22	AAZ11053	Human stem cell fa	472	10.6	36.6	24	ABK16688	Leptin receptor (L
400	10.6	36.6	21	22	AAZ11053	Human stem cell fa	473	10.6	36.6	24	ABK16688	Leptin receptor (L
401	10.6	36.6	21	22	AAZ11053	Human stem cell fa	474	10.6	36.6	24	ABK16688	Leptin receptor (L
402	10.6	36.6	21	22	AAZ11053	Human stem cell fa	475	10.6	36.6	24	ABK16688	Leptin receptor (L
403	10.6	36.6	21	22	AAZ11053	Human stem cell fa	476	10.6	36.6	24	ABK16688	Leptin receptor (L
404	10.6	36.6	21	22	AAZ11053	Human stem cell fa	477	10.6	36.6	24	ABK16688	Leptin receptor (L
405	10.6	36.6	21	22	AAZ11053	Human stem cell fa	478	10.6	36.6	24	ABK16688	Leptin receptor (L
406	10.6	36.6	21	22	AAZ11053	Human stem cell fa	479	10.6	36.6	24	ABK16688	Leptin receptor (L
407	10.6	36.6	21	22	AAZ11053	Human stem cell fa	480	10.6	36.6	24	ABK16688	Leptin receptor (L
408	10.6	36.6	21	22	AAZ11053	Human stem cell fa	481	10.6	36.6	24	ABK16688	Leptin receptor (L
409	10.6	36.6	21	22	AAZ11053	Human stem cell fa	482	10.6	36.6	24	ABK16688	Leptin receptor (L
410	10.6	36.6	21	22	AAZ11053	Human stem cell fa	483	10.6	36.6	24	ABK16688	Leptin receptor (L
411	10.6	36.6	21	22	AAZ11053	Human stem cell fa	484	10.6	36.6	24	ABK16688	Leptin receptor (L
412	10.6	36.6	21	22	AAZ11053	Human stem cell fa	485	10.6	36.6	24	ABK16688	Leptin receptor (L
413	10.6	36.6	21	22	AAZ11053	Human stem cell fa	486	10.6	36.6	24	ABK16688	Leptin receptor (L
414	10.6	36.6	21	22	AAZ11053	Human stem cell fa	487	10.6	36.6	24	ABK16688	Leptin receptor (L
415	10.6	36.6	21	22	AAZ11053	Human stem cell fa	488	10.6	36.6	24	ABK16688	Leptin receptor (L
416	10.6	36.6	21	22	AAZ11053	Human stem cell fa	489	10.6	36.6	24	ABK16688	Leptin receptor (L
417	10.6	36.6	21	22	AAZ11053	Human stem cell fa	490	10.6	36.6	24	ABK16688	Leptin receptor (L
418	10.6	36.6	21	22	AAZ11053	Human stem cell fa	491	10.6	36.6	24	ABK16688	Leptin receptor (L
419	10.6	36.6	21	22	AAZ11053	Human stem cell fa	492	10.6	36.6	24	ABK16688	Leptin receptor (L
420	10.6	36.6	21	22	AAZ11053	Human stem cell fa	493	10.6	36.6	24	ABK16688	Leptin receptor (L
421	10.6	36.6	21	22	AAZ11053	Human stem cell fa	494	10.6	36.6	24	ABK16688	Leptin receptor (L
422	10.6	36.6	21	22	AAZ11053	Human stem cell fa	495	10.6	36.6	24	ABK16688	Leptin receptor (L
423	10.6	36.6	21	22	AAZ11053	Human stem cell fa	496	10.6	36.6	24	ABK16688	Leptin receptor (L
424	10.6	36.6	21	22	AAZ11053	Human stem cell fa	497	10.6	36.6	24	ABK16688	Leptin receptor (L
425	10.6	36.6	21	22	AAZ11053	Human stem cell fa	498	10.6	36.6	24	ABK16688	Leptin receptor (L
426	10.6	36.6	21	22	AAZ11053	Human stem cell fa	499	10.6	36.6	24	ABK16688	Leptin receptor (L
427	10.6	36.6	21	22	AAZ11053	Human stem cell fa	500	10.6	36.6	24	ABK16688	Leptin receptor (L
428	10.6	36.6	21	22	AAZ11053	Human stem cell fa	501	10.6	36.6	24	ABK16688	Leptin receptor (L
429	10.6	36.6	21	22	AAZ11053	Human stem cell fa	502	10.6	36.6	24	ABK16688	Leptin receptor (L
430	10.6	36.6	21	22	AAZ11053	Human stem cell fa	503	10.6	36.6	24	ABK16688	Leptin receptor (L
431	10.6	36.6	21	22	AAZ11053	Human stem cell fa	504	10.6	36.6	24	ABK16688	Leptin receptor (L
432	10.6	36.6	21	22	AAZ11053	Human stem cell fa	505	10.6	36.6	24	ABK16688	Leptin receptor (L
433	10.6	36.6	21	22	AAZ11053	Human stem cell fa	506	10.6	36.6	24	ABK16688	Leptin receptor (L
434	10.6	36.6	21	22	AAZ11053	Human stem cell fa	507	10.6	36.6	24	ABK16688	Leptin receptor (L
435	10.6	36.6	21	22	AAZ11053	Human stem cell fa	508	10.6	36.6	24	ABK16688	Leptin receptor (L
436	10.6	36.6	21	22	AAZ11053	Human stem cell fa	509	10.6	36.6	24	ABK16688	Leptin receptor (L
437	10.6	36.6	21	22	AAZ11053	Human stem cell fa	510	10.6	36.6	24	ABK16688	Leptin receptor (L
438	10.6	36.6	21	22	AAZ11053	Human stem cell fa	511	10.6	36.6	24	ABK16688	Leptin receptor (L
439	10.6	36.6	21	22	AAZ11053	Human stem cell fa	512	10.6	36.6	24	ABK16688	Leptin receptor (L
440	10.6	36.6	21	22	AAZ11053	Human stem cell fa	513	10.6	36.6	24	ABK16688	Leptin receptor (L
441	10.6	36.6	21	22	AAZ11053	Human stem cell fa	514	10.6	36.6	24	ABK16688	Leptin receptor (L
442	10.6	36.6	21	22	AAZ11053	Human stem cell fa	515	10.6	36.6	24	ABK16688	Leptin receptor (L
443	10.6	36.6	21	22	AAZ11053	Human stem cell fa	516	10.6	36.6	24	ABK16688	Leptin receptor (L
444	10.6	36.6	21	22	AAZ11053	Human stem cell fa	517	10.6	36.6	24	ABK16688	Leptin receptor (L
445	10.6	36.6	21	22	AAZ11053	Human stem cell fa	518	10.6	36.6	24	ABK16688	Leptin receptor (L
446	10.6	36.6	21	22	AAZ11053	Human stem cell fa	519	10.6	36.6	24	ABK16688	Leptin receptor (L
447	10.6	36.6	21	22	AAZ11053	Human stem cell fa	520	10.6	36.6	24	ABK16688	Leptin receptor (L

CryIA(a) PCR prime
 Bacillus thuringie
 Primer 11 for age1
 PCR primer used to
 B. thuringiensis i
 Leptin receptor (L
 Leptin receptor (L
 Oligo #2 to produc
 Helicobacter pylor
 Chemically synthe
 HHV-6 associated m
 DNA polymerase I 5
 T. thermohydrosulf
 HIV-1 env (non-cle
 HIV-1 env (non-cle
 PCR primer HIVNT1
 PCR primer HIVNT1
 Primer pr 2B for s
 Human map-related
 Human map-related
 Human map-related
 Human map-related
 Human map-related
 Human map-related
 Human factor VIII
 Oligo 20. to const
 CNS disorder-relat
 CNS disorder-relat
 Pneumocystis carin
 Probe 1159 for P.
 Yeast GAL4 specifi
 Staphylococcus aur
 Human SNP oligonuc
 Human SNP oligonuc
 Mouse IL-5 hammerh
 IGF-1 oligonucleot
 Human biallelic ma
 PCR primer used to
 HPV11 typing probe
 Small E6 amplified
 HPV typing probe W
 Human papillomavir
 Human chromosome 1
 Probe WD134 for hu
 PCR primer for hum
 Mouse caspase 8 mR
 Mouse caspase 8 mR
 Human bcl-6 phosph
 Interferon IFN-gam
 Primer OT6147 for
 Primer #1 to ampli
 Sense PCR primer u
 GATA-1 locus splic
 Human biallelic ma
 Interferon gamma (Rat G protein, Gi-
 Human apolipoprote
 Oligonucleotide SE
 Human ngPCR56 PCR
 Reverse PCR primer
 Human osteoregulin
 Primer #4 used in
 Mouse BR96 recepto
 Mouse BR96 recepto
 Human dihydroorota
 Probe for identify
 HLA DpB1 gene PCR
 Dog genomic marker
 PCR primer for cDN
 Chromosome 11 (loc
 Mouse fit-1 VEGF r
 Mouse fit-1 VEGF r
 Mouse fit-1 VEGF r
 Mouse fit-1 VEGF r

521	10.4	35.9	27	18	AAV72365	Mouse flk-1 VEGF r
522	10.4	35.9	27	18	AAV72083	Mouse flk-1 VEGF r
523	10.4	35.9	27	18	AAV72016	Mouse flk-1 VEGF r
524	10.4	35.9	27	18	AAV70754	Human KDR VEGF rec
525	10.4	35.9	27	18	AAV70582	Human KDR VEGF rec
526	10.4	35.9	27	18	AAV68849	Human flt1 VEGF re
527	10.4	35.9	27	18	AAV67748	Human flt1 VEGF re
528	10.4	35.9	27	18	AAV67336	Human flt1 VEGF re
529	10.4	35.9	27	22	AAV39846	SNP specific lower
530	10.4	35.9	28	22	AAV24058	P. falciparum PfEM
531	10.4	35.9	28	22	AAV15820	Human prostate spe
532	10.4	35.9	28	22	AAV39425	SNP specific upper
533	10.4	35.9	29	16	AAV05510	Interferon-gamma 5
534	10.4	35.9	29	16	AAV6994	Interferon-gamma p
535	10.4	35.9	29	20	AAV2282	Interferon-gamma (
536	10.4	35.9	29	20	AAV2977	Human B-raf hammet
537	10.4	35.9	29	22	AAV05585	Interferon-gamma c
538	10.4	35.9	30	20	AAV2984	Anti-Staph (HAY) 9
539	10.4	35.9	30	21	AAV27960	Probe ZC12353 for
540	10.4	35.9	30	22	AAV88048	PCR primer INFFOR
541	10.4	35.9	30	22	AAV88105	H. pylori catalase
542	10.4	35.9	31	19	AAV67575	H. pylori catalase
543	10.4	35.9	31	19	AAV39042	Nucleotide fragmen
544	10.4	35.9	31	20	AAV39042	Human genomic DNA
545	10.4	35.9	32	21	AAV29495	Primer KC93 used
546	10.4	35.9	32	21	AAV29495	Primer KC94 used
547	10.4	35.9	33	16	AAV086110	PCR primer for HAR
548	10.4	35.9	33	24	AAV14958	Human cytochrome-c
549	10.4	35.9	33	24	AAV045083	Human uterine glob
550	10.4	35.9	34	19	AAV45083	Human IL-12 primer
551	10.4	35.9	35	15	AAV73539	PCR primer V-OLT#5
552	10.4	35.9	35	17	AAV43059	Murine gamma inter
553	10.4	35.9	35	17	AAV35663	Murine gamma inter
554	10.4	35.9	35	18	AAV73341	Primer #2 for mut1
555	10.4	35.9	35	18	AAV73341	Primer for rat HRP
556	10.4	35.9	35	18	AAV78350	Chimeric MVA vacci
557	10.4	35.9	35	20	AAV18003	Human HRP1 gene pr
558	10.4	35.9	35	20	AAV03469	PCR primer for nuc
559	10.4	35.9	36	18	AAV09729	Adenovirus mitogen
560	10.4	35.9	36	22	AAV56646	Human gamma interf
561	10.4	35.9	36	24	AAV82765	Human protective D
562	10.4	35.9	37	7	AAV60808	Alpaz2 controllabl
563	10.4	35.9	39	13	AAV2821	Predetermined olig
564	10.4	35.9	39	21	AAV2821	Mouse caspase-8 DE
565	10.4	35.9	39	21	AAV2821	T cell antigen rec
566	10.4	35.9	40	12	AAV2302	HPV type 11-specif
567	10.4	35.9	40	15	AAV73058	PCR primer for hum
568	10.4	35.9	40	17	AAV73061	Human gamma interf
569	10.4	35.9	40	17	AAV73061	Human gamma interf
570	10.4	35.9	40	18	AAV71162	HPV type 11 probe
571	10.4	35.9	41	21	AAV68538	Pansy petal AR-AR
572	10.4	35.9	41	21	AAV68538	Lipocortin SNP pro
573	10.4	35.9	41	24	AAV14961	Human cytochrome-c
574	10.4	35.9	41	24	AAV14961	Human cytochrome-c
575	10.4	35.9	42	17	AAV83918	Human uterine glob
576	10.4	35.9	42	17	AAV83918	5' primer for RT-P
577	10.4	35.9	42	18	AAV40016	CFTR exon 11 PCR p
578	10.4	35.9	42	18	AAV40016	Reverse primer P4
579	10.4	35.9	42	21	AAV74655	Adenovirus mitogen
580	10.4	35.9	44	18	AAV09730	CFTR gene exon 11
581	10.4	35.9	45	19	AAV09940	Reverse primer P4
582	10.4	35.9	45	19	AAV09940	Human map-related
583	10.4	35.9	45	21	AAV90015	Human map-related
584	10.4	35.9	47	21	AAV65984	Human SNP oligonuc
585	10.4	35.9	50	22	AAV34019	Human SNP oligonuc
586	10.4	35.9	50	22	AAV34019	RSV N hammerhead r
587	10.2	35.2	15	16	AAV57251	RSV N hammerhead r
588	10.2	35.2	15	16	AAV57251	RSV IB hammerhead r
589	10.2	35.2	15	16	AAV57251	Plasmid pF3 constr
590	10.2	35.2	15	20	AAV28142	Human wild-type EA
591	10.2	35.2	15	21	AAV93248	Primer used in con
592	10.2	35.2	17	18	AAV71011	Human KDR VEGF rec
593	10.2	35.2	17	18	AAV71011	Human KDR VEGF rec
594	10.2	35.2	17	18	AAV71012	Human KDR VEGF rec
595	10.2	35.2	17	18	AAV7539	Human EGF-R target
596	10.2	35.2	17	19	AAV97540	Human EGF-R target
597	10.2	35.2	17	19	AAV97541	Human EGF-R target
598	10.2	35.2	17	19	AAV97541	Solandine glucosy
599	10.2	35.2	17	21	AAV235359	Antisense primer f
600	10.2	35.2	17	23	AAV00599	Human NOO Hammet
601	10.2	35.2	18	21	AAV75132	E. carotovora nucle
602	10.2	35.2	18	21	AAV75132	Human biallelic ma
603	10.2	35.2	19	17	AAV7245	pNA fragment U8 us
604	10.2	35.2	19	17	AAV7245	pNA fragment U6 us
605	10.2	35.2	19	17	AAV7245	DNA component of D
606	10.2	35.2	19	17	AAV7245	DNA component of R
607	10.2	35.2	19	17	AAV7245	DNA component of R
608	10.2	35.2	19	17	AAV7245	RNA component of R
609	10.2	35.2	19	17	AAV7245	RNA component of R
610	10.2	35.2	19	21	AAV83202	cdk7 ribozyme bind
611	10.2	35.2	19	22	AAV83260	Human XPF-XPA cDNA
612	10.2	35.2	19	22	AAV83260	Human Nuc-XPA cDNA
613	10.2	35.2	20	12	AAV58364	Cell-cycle depende
614	10.2	35.2	20	12	AAV58364	Primer for human 1
615	10.2	35.2	20	14	AAV39530	PCR primer #2 for
616	10.2	35.2	20	14	AAV39530	Primer derived fro
617	10.2	35.2	20	14	AAV39530	Primer derived fro
618	10.2	35.2	20	14	AAV39530	Probe H for retino
619	10.2	35.2	20	18	AAV91679	Hepatocyte growth
620	10.2	35.2	20	20	AAV03291	PCR primer used to
621	10.2	35.2	20	20	AAV03291	PCR primer used to
622	10.2	35.2	20	20	AAV03291	PCR primer used to
623	10.2	35.2	20	20	AAV03291	PCR primer used to
624	10.2	35.2	20	20	AAV03291	PCR primer used to
625	10.2	35.2	20	22	AAV10560	Oculocutaneous alb
626	10.2	35.2	20	22	AAV10560	Human caspase 3 an
627	10.2	35.2	21	22	AAV09119	Human hCRBP-1so RT
628	10.2	35.2	21	22	AAV09119	Tumour necrosis fa
629	10.2	35.2	21	22	AAV09119	A. oryzae prf gen
630	10.2	35.2	21	22	AAV09119	Human aldehyde de
631	10.2	35.2	21	22	AAV09119	Human ALDH21 PCR p
632	10.2	35.2	21	22	AAV09119	Human gene single
633	10.2	35.2	21	22	AAV09119	Human IGRB coding
634	10.2	35.2	21	22	AAV09119	Rat protein kinase
635	10.2	35.2	22	20	AAV231624	PCR primer for hum
636	10.2	35.2	22	20	AAV231624	Human spastin ORF
637	10.2	35.2	22	22	AAV20138	K-ras MTO-PCR prim
638	10.2	35.2	23	15	AAV66486	Human g protein co
639	10.2	35.2	23	19	AAV40942	Primer TELATL1:871
640	10.2	35.2	23	19	AAV40942	PCR primer used to
641	10.2	35.2	23	19	AAV40942	NBCS (PNC) gene e
642	10.2	35.2	23	19	AAV40942	Multiplex PCR prim
643	10.2	35.2	23	20	AAV22870	Human CYP2A7 probe
644	10.2	35.2	23	20	AAV22870	Downstream PCR prl
645	10.2	35.2	24	13	AAV75130	E. carotovora nucle
646	10.2	35.2	24	16	AAV75130	Borrelia sp. rRNA
647	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
648	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
649	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
650	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
651	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
652	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
653	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
654	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
655	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
656	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
657	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
658	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
659	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
660	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
661	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
662	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
663	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
664	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
665	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA
666	10.2	35.2	24	17	AAV75130	Borrelia sp. rRNA

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Accession	Gene	Protein	Length	Score	Value	Gene	Protein	Length	Score	Value
667	CTFR gene analysis	blaoA10 resistanc	10.2	35.2	26	21	AA06064	41	20	AAV79894
668	PCR primer OUL22.	Human protein secr	10.2	35.2	26	22	AAH01446	41	21	AAA92994
669	PCR primer GFP-Eco	Na+ and H+ antipor	10.2	35.2	26	22	AA02034	41	22	AAI69966
670	PCR primer GFP-Eco	Borrelia sp. rRNA	10.2	35.2	26	24	AA02034	41	22	AA03151
671	PCR primer GFP-Eco	B2 bradykinin rece	10.2	35.2	27	21	AA02034	42	19	AAV59313
672	PCR primer GFP-Eco	Human biallelic po	10.2	35.2	27	17	AAAT72936	42	20	AAZ21029
673	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	17	AAAT72936	42	22	AAI64377
674	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ06983
675	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
676	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
677	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
678	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
679	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
680	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
681	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
682	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
683	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
684	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
685	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
686	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
687	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
688	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
689	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
690	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
691	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
692	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
693	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
694	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
695	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
696	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
697	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
698	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
699	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
700	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT72936	42	20	AAZ04459
701	PCR primer GFP-Eco	PCR primer used to	10.2	35.2	28	19	AAAT729			

[illegible]

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c 959 10 34.5 43 20 AAX91971
 c 960 10 34.5 43 21 AAX64765
 c 961 10 34.5 43 22 AAX56268
 c 962 10 34.5 44 16 AAX94911
 c 963 10 34.5 44 16 AAX94912
 c 964 10 34.5 44 20 AAX97741
 c 965 10 34.5 44 22 AAD18014
 c 966 10 34.5 45 17 AAT27250
 c 967 10 34.5 45 17 AAT18488
 c 968 10 34.5 45 22 AAX90926
 c 969 10 34.5 45 22 AAC89589
 c 970 10 34.5 46 17 AAZ27347
 c 971 10 34.5 46 20 AAZ23234
 c 972 10 34.5 46 22 AAD09000
 c 973 10 34.5 46 22 AAD09028
 c 974 10 34.5 46 22 AAX41738
 c 975 10 34.5 47 15 AAG69399
 c 976 10 34.5 47 18 AAT63861
 c 977 10 34.5 47 20 AAZ01052
 c 978 10 34.5 47 20 AAX17149
 c 979 10 34.5 47 21 AAZ65974
 c 980 10 34.5 47 21 AAZ66334
 c 981 10 34.5 47 21 AAZ66376
 c 982 10 34.5 47 21 AAZ66481
 c 983 10 34.5 47 21 AAZ66566
 c 984 10 34.5 47 21 AAZ66641
 c 985 10 34.5 47 21 AAZ66676
 c 986 10 34.5 47 21 AAZ66705
 c 987 10 34.5 47 21 AAZ66749
 c 988 10 34.5 47 21 AAZ66890
 c 989 10 34.5 47 21 AAZ67155
 c 990 10 34.5 47 21 AAZ67637
 c 991 10 34.5 47 21 AAZ67785
 c 992 10 34.5 47 21 AAZ67814
 c 993 10 34.5 47 21 AAZ67823
 c 994 10 34.5 47 21 AAZ67865
 c 995 10 34.5 47 21 AAZ67902
 c 996 10 34.5 47 21 AAZ67933
 c 997 10 34.5 47 21 AAZ67981
 c 998 10 34.5 47 21 AAZ68082
 c 999 10 34.5 47 21 AAZ68508
 c 1000 10 34.5 47 21 AAZ68679

ALIGNMENTS

RESULT 1
 AAX37776
 ID AAX37776 standard; DNA; 19 BP.
 AC AAX37776;
 XX 09-JUL-1999 (first entry)
 XX Staphylococcus sp. detecting oligonucleotide femA1.
 DE
 DE FemA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS
 OS Synthetic.
 OS Staphylococcus sp.
 XX WO9916780-A2.
 XX
 XX 08-APR-1999.
 XX 28-SEP-1998; 98WO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.

XX Gala J, Vannuffel P;
 PI WPI; 1999-287521/24.
 XX New Staphylococcus-specific oligonucleotides
 DR
 DR Claim 5; Page 9; 48pp; English.
 XX
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 XX Sequence 19 BP; 9 A; 1 C; 3 G; 5 T; 0 other;

Query Match 65.5%; Score 19; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 atgaattacagagttaa 26
 |||||
 Db 1 atgaattacagagttaa 19

RESULT 2
 AAX37792/C
 ID AAX37792 standard; DNA; 29 BP.
 XX
 AC AAX37792;
 XX 09-JUL-1999 (first entry)
 XX Staphylococcus sp. detecting oligonucleotide 27.

XX FemA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS
 OS Synthetic.
 OS Staphylococcus sp.
 XX WO9916780-A2.
 XX
 XX 08-APR-1999.
 XX 28-SEP-1998; 98WO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.

XX Gala J, Vannuffel P;
 XX WPI; 1999-287521/24.
 XX New Staphylococcus-specific oligonucleotides
 XX
 XX Example 1; Fig 1; 48pp; English.

XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to

CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various feta
 CC sequences which are specific to known or unknown *Staphylococci* species.
 CC Since the feta sequence is similar to the feta sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of feta
 CC genes of different *Staphylococci* species or other gram-positive bacteria.
 CC The feta nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the feta
 CC nucleic acid sequences. They can also be used for producing vaccines
 CC against *Staphylococci* infections.

CC
 CC Sequence 29 BP; 8 A; 5 C; 2 G; 14 T; 0 other;

Query Match 62.1%; Score 18; DB 20; Length 29;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 tgaattacagagtaa 26
 |||||||
 DB 29 TGAATTACAGAGTTAA 12

RESULT 3
 AAH39954/c
 ID AAH39954 standard; DNA; 27 BP.

XX AAH39954;

XX 14-AUG-2001 (first entry)

DE SNP specific lower PCR primer SEQ ID 2750.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KW Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.

XX Homo sapiens.

OS W0200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000MO-US28436.

XX 15-OCT-1999; 99US-0160096.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

DR New genotyping oligonucleotide, useful for detecting the presence.
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample -

XX Claim 1; Page 64; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNP) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or

CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence.

CC
 CC Sequence 27 BP; 5 A; 9 C; 1 G; 12 T; 0 other;

Query Match 48.3%; Score 14; DB 22; Length 27;
 Best Local Similarity 100.0%; Pred. No. 24e03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 tgaattacagag 22
 |||||||
 DB 19 TGAATTACAGAG 6

RESULT 4
 AAH3029/c
 ID AAH3029 standard; CDNA; 33 BP.

XX AAH3029;

XX 18-NOV-1998 (first entry)

DE Dirofilaria immitis transglutaminase DNA ndITG143 antisense primer.

XX Dirofilaria immitis transglutaminase; Tg; parasitic nematode infection;

KW Brugia malayi transglutaminase; Onchocerca volvulus transglutaminase;

KW PCR; primer; amplification; ss.

XX Synthetic.

OS Dirofilaria immitis.

XX W09824887-A2.

XX 11-JUN-1998.

XX 02-DEC-1997; 97WO-US21999.

XX 03-DEC-1996; 96US-0781420.

XX (HESK-) HESKA CORP.

XX Chandrasekar R, Mehta K;

XX WPI; 1998-333309/29.

DR New isolated parasitic nematode transglutaminase genes - used to
 PT develop products for the detection, prevention and treatment of
 PT infections by parasitic nematodes

XX Example 10; Page 63; 129pp; English.

XX The antisense and sense (AAV33028) primers were used to amplify
 CC a Dirofilaria immitis transglutaminase (TG) DNA molecule, denoted
 CC ndITG143, from D. immitis adult female CDNA. The sequence of ndITG143
 CC was found to overlap with that of ndITG1472 (see AAV33025-V33027) and
 CC ndITG1407 (see AAV33030 and AAV33031), allowing the construction of a
 CC full length D. immitis TG encoding DNA sequence denoted as ndITG1881
 CC (AAV33017 and AAV33033). The ndITG1881 DNA sequence encodes a 495
 CC residue TG protein (AAW0270). The invention also claims for TG protein
 CC sequences and the corresponding DNA sequences encoding these proteins

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC isolated from Brugia malayi (AAV33018, AAV33019, AAW70271 and AAW70272)
CC and Onchocerca volvulus (AAV33020 and AAW70273). The nematode TG DNA and
CC protein sequences are claimed to be useful for the diagnosis, prevention
CC and treatment of parasitic nematode infection.
XX
SQ Sequence 33 BP; 7 A; 10 C; 4 G; 12 T; 0 other;

Query Match 48.3%; Score 14; DB 19; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
|||||
DB 33 ATGAATTACAGA 20

RESULT 5
AAV33030
ID AAV33030 standard; cDNA; 33 BP.

XX AAV33030;

XX 18-NOV-1998 (first entry)

XX Dirofilaria immitis transglutaminase DNA nDITG1407 sense primer.

XX Dirofilaria immitis transglutaminase; TG; parasitic nematode infection;
KW Brugia malayi transglutaminase; Onchocerca volvulus transglutaminase;
KW PCR; primer; amplification; ss.

XX Synthetic.

XX Dirofilaria immitis.

XX WO9824887-A2.

XX 11-JUN-1998.

XX 02-DEC-1997; 97WO-US21999.

XX 03-DEC-1998; 96US-0781420.

XX (HESK-) HESKA CORP.

XX Chandrashekar R, Mehta K;

XX WPI; 1998-333309/29.

XX New isolated parasitic nematode transglutaminase genes - used to
PT develop products for the detection, prevention and treatment of
PT infections by parasitic nematodes

XX Example 11; Page 64; 129pp; English.

XX The sense and antisense (AAV33031) primers were used to amplify
CC a Dirofilaria immitis transglutaminase (TG) DNA molecule, denoted
CC nDITG1407, from D. immitis adult female cDNA. The sequence of
CC nDITG1407 was found to overlap with that of nDITG1472 (see AAV33025-
CC AAV33027) and nDITG143 (see AAV33028 and AAV33029), allowing the
CC construction of a full length D. immitis TG encoding DNA sequence denoted
CC as nDITG1881 (AAV33017 and AAV33033). The nDITG1881 DNA sequence encodes
CC a 495 residue TG protein (AAW70270). The invention also claims for TG
CC protein sequences and the corresponding DNA sequences encoding these
CC proteins isolated from Brugia malayi (AAV33018, AAV33019, AAW70271 and
CC AAW70272) and Onchocerca volvulus (AAV33020 and AAW70273). The nematode
CC TG DNA and protein sequences are claimed to be useful for the diagnosis,
CC prevention and treatment of parasitic nematode infection.

XX Sequence 33 BP; 11 A; 7 C; 9 G; 6 T; 0 other;

Query Match 48.3%; Score 14; DB 19; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
|||||
DB 13 atgaattacaga 26

RESULT 6

AAI67837/C

ID AAI67837 standard; DNA; 33 BP.

XX AAI67837;

XX 27-FEB-2002 (first entry)

XX D. immitis transglutaminase cDNA amplifying antisense primer.

XX Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
KW nematode; heartworm; PCR primer; ss.

XX Dirofilaria immitis.

XX US6309644-B1.

XX 30-OCT-2001.

XX 12-JUN-1997; 97US-0874102.

XX 03-DEC-1996; 96US-0781420.

XX (HESK-) HESKA CORP.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Chandrashekar R, Mehta K;

XX WPI; 2002-040231/05.

XX Novel Dirofilaria immitis transglutaminase protein which also has
PT protein disulfide isomerase activity, used to identify transglutaminase
PT activity inhibitors that are useful for protecting animals from
PT heartworm

XX Example 10; Column 43; 66pp; English.

XX The invention relates to parasitic nematode transglutaminase proteins and
CC polynucleotides encoding them. The transglutaminase proteins are useful
CC for identifying a compound capable of inhibiting transglutaminase or
CC protein disulfide isomerase activity. The proteins represent novel
CC targets for antiparasite vaccines and drugs. The products inhibit the
CC crucial steps in nematode molting that involve nematode transglutaminase.
CC The proteins are also useful for preventing an animal (a dog) from
CC heartworm, a disease condition caused by D. immitis. The nematode protein
CC disulfide isomerase or transglutaminase activity inhibitors identified
CC are useful for protecting an animal from heartworm. The proteins are
CC useful as diagnostic agents to detect infection by parasitic nematodes.
CC Sequences AAI67836-39 represent PCR primers for amplifying nematode
CC transglutaminase nucleic acid molecules from D. immitis female adult
CC cDNA library.

XX Sequence 33 BP; 7 A; 10 C; 4 G; 12 T; 0 other;

Query Match 48.3%; Score 14; DB 24; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21

|||||

DB 33 ATGAATTACAGA 20

RESULT 7

AAI67838

```

ID  AA167838 standard; DNA; 33 BP.
XX
XX  AA167838;
AC
XX  27-FEB-2002 (first entry)
DT
XX
XX  D. immitis transglutaminase cDNA amplifying sense primer.
DE
XX
XX  Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
KW  nematode; heartworm; PCR primer; ss.
XX
XX  Dirofilaria immitis.
OS
XX  US6309644-B1.
PN
XX  30-OCT-2001.
PD
XX  12-JUN-1997; 97US-0874102.
PF
XX  03-DEC-1996; 96US-0781420.
PR
XX
XX  (HESK-) HESKA CORP.
PA  (TEXA) UNIV TEXAS SYSTEM.
XX
XX  Chandrashekar R, Mehta K;
PI
XX  WPI; 2002-040231/05.
DR
XX
XX  Novel Dirofilaria immitis transglutaminase protein which also has
PT  protein disulfide isomerase activity, used to identify transglutaminase
PT  activity inhibitors that are useful for protecting animals from
PT  heartworm.
XX
XX  Example 11; Column 43; 66pp; English.
PS
XX  The invention relates to parasitic nematode transglutaminase proteins and
XX  polynucleotides encoding them. The transglutaminase proteins are useful
XX  for identifying a compound capable of inhibiting transglutaminase or
XX  protein disulfide isomerase activity. The proteins represent novel
XX  targets for antiparasite vaccines and drugs. The products inhibit the
XX  crucial steps in nematode molting that involve nematode transglutaminase.
XX  Crucial steps are also useful for preventing an animal (a dog) from
XX  heartworm, a disease condition caused by D. immitis. The nematode protein
XX  disulfide isomerase or transglutaminase activity inhibitors identified
XX  are useful for protecting an animal from heartworm. The proteins are
XX  useful as diagnostic agents to detect infection by parasitic nematodes.
XX  Sequences AA167835-39 represent PCR primers for amplifying nematode
XX  transglutaminase nucleic acid molecules from D. immitis female adult
XX  cDNA library.
XX
XX  Sequence 33 BP; 11 A; 7 C; 9 G; 6 T; 0 other;
SO

```

```

Query Match      48.3%; Score 14; DB 24; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY  8 atgaattacaga 21
    |||
DB  13 atgaattacaga 26

```

RESULT 8

AA167859 standard; cDNA; 45 BP.

```

XX
XX  AA167859;
AC
XX  27-FEB-2002 (first entry)
DT
XX
XX  D. immitis transglutaminase protein PD1NG15 coding sequence.
DE
XX  Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
KW

```

```

KM  nematode; heartworm; ss.
XX
XX  Dirofilaria immitis.
OS
XX  Key Location/Qualifiers
XX  CDS 1..45
XX  FT /*tag= a
XX  FT /product= "mature transglutaminase"
XX
XX  US6309644-B1.
PN
XX  30-OCT-2001.
PD
XX  12-JUN-1997; 97US-0874102.
PF
XX  03-DEC-1996; 96US-0781420.
PR
XX
XX  (HESK-) HESKA CORP.
PA  (TEXA) UNIV TEXAS SYSTEM.
XX
XX  Chandrashekar R, Mehta K;
PI
XX  WPI; 2002-040231/05.
DR
XX  P-PSDB; AAG66112.
DR
XX
XX  Novel Dirofilaria immitis transglutaminase protein which also has
PT  protein disulfide isomerase activity, used to identify transglutaminase
PT  activity inhibitors that are useful for protecting animals from
PT  heartworm.
XX
XX  Claim 3; Columns 113-114; 66pp; English.
PS
XX
XX  The invention relates to parasitic nematode transglutaminase proteins and
XX  polynucleotides encoding them. The transglutaminase proteins are useful
XX  for identifying a compound capable of inhibiting transglutaminase or
XX  protein disulfide isomerase activity. The proteins represent novel
XX  targets for antiparasite vaccines and drugs. The products inhibit the
XX  crucial steps in nematode molting that involve nematode transglutaminase.
XX  Crucial steps are also useful for preventing an animal (a dog) from
XX  heartworm, a disease condition caused by D. immitis. The nematode protein
XX  disulfide isomerase or transglutaminase activity inhibitors identified
XX  are useful for protecting an animal from heartworm. The proteins are
XX  useful as diagnostic agents to detect infection by parasitic nematodes.
XX  The present sequence represents a D. immitis nucleotide sequence encoding
XX  a transglutaminase protein PD1NG15, the mature form of PD1NG40.
XX
XX  Sequence 45 BP; 14 A; 5 C; 16 G; 10 T; 0 other;
SO

```

```

Query Match      48.3%; Score 14; DB 24; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY  8 atgaattacaga 21
    |||
DB  13 atgaattacaga 26

```

AA167860 standard; cDNA; 45 BP.

```

XX
XX  AA167860;
AC
XX  27-FEB-2002 (first entry)
DT
XX
XX  Complementary strand of transglutaminase protein PD1NG15 coding DNA.
DE
XX  Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
KW  nematode; heartworm; ss.
XX
XX  Dirofilaria immitis.
OS

```

XX	21-JUN-2000; 2000WO-AU00693.
PF	
XX	
XX	21-JUN-1999; 99US-0140345.
PR	
XX	(MURD-) MURDOCH CHILDRENS RES INST.
PA	
XX	
PI	Wright CJ, Werther GA, Edmondson SR;
XX	
XX	WPI; 2001-041421/05.
DR	
XX	Ameliorating the effects of a disorder, e.g. psoriasis, by
XX	administering UV (ultra-violet) treatment (optional) and an antisen-
PT	nucleic acid that inhibits or reduces growth factor mediated cell
PT	proliferation and/or inflammation -
PT	
XX	
XX	Example 8; Page 91; 20pp; English.
PS	
XX	The present invention relates to a method for ameliorating the effects
XX	of skin disorders. The method comprises contacting the skin with an
CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP), which is capable of
CC	inhibiting or reducing growth factor mediated cell proliferation,
CC	inflammation and/or other disorders. The present sequence is an
CC	oligonucleotide which can be used to design the antisense
CC	oligonucleotides of the present invention (see AAF45151 and
CC	AAF45153-F45161). The method is useful for ameliorating the effects of
CC	psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC	keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC	skin, a hyperneovascular condition such as a neovascular condition of the
CC	retina, brain or skin, growth factor-mediated malignancies, other
CC	sclerotic disease, kidney disease, hyperproliferation of the inside of
CC	blood vessels or any other hyperplasia.
XX	Sequence 15 BP; 8 A; 1 C; 2 G; 4 T; 0 other;
SQ	

Query Match 46.2%; Score 13.4; DB 22; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 atgaattaccagag 22
 | | | | | | | | | |
Db 1 atgaattaccagag 15

RESULT 11
AA83773
ID AA83773 standard; DNA; 19 BP.
XX
AC AA83773;
XX
DT 04-DEC-2000 (first entry).
XX
DE cdk-we-hu ribozyme binding site #248.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW restenosis; ss.
XX
OS Mammalia.
XX
FN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-O110954.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX

XX	21-JUN-2000; 2000WO-AU00693.
PF	
XX	
XX	21-JUN-1999; 99US-0140345.
PR	
XX	(MURD-) MURDOCH CHILDRENS RES INST.
PA	
XX	
PI	Wright CJ, Werther GA, Edmondson SR;
XX	
XX	WPI; 2001-041421/05.
DR	
XX	Ameliorating the effects of a disorder, e.g. psoriasis, by
XX	administering UV (ultra-violet) treatment (optional) and an antisen-
PT	nucleic acid that inhibits or reduces growth factor mediated cell
PT	proliferation and/or inflammation -
PT	
XX	
XX	Example 8; Page 91; 20pp; English.
PS	
XX	The present invention relates to a method for ameliorating the effects
XX	of skin disorders. The method comprises contacting the skin with an
CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP), which is capable of
CC	inhibiting or reducing growth factor mediated cell proliferation,
CC	inflammation and/or other disorders. The present sequence is an
CC	oligonucleotide which can be used to design the antisense
CC	oligonucleotides of the present invention (see AAF45151 and
CC	AAF45153-F45161). The method is useful for ameliorating the effects of
CC	psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC	keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC	skin, a hyperneovascular condition such as a neovascular condition of the
CC	retina, brain or skin, growth factor-mediated malignancies, other
CC	sclerotic disease, kidney disease, hyperproliferation of the inside of
CC	blood vessels or any other hyperplasia.
XX	Sequence 15 BP; 8 A; 1 C; 2 G; 4 T; 0 other;
SQ	

Query Match 46.2%; Score 13.4; DB 22; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 atgaattaccagag 22
 | | | | | | | | | |
Db 1 atgaattaccagag 15

RESULT 11
AA83773
ID AA83773 standard; DNA; 19 BP.
XX
AC AA83773;
XX
DT 04-DEC-2000 (first entry).
XX
DE cdk-we-hu ribozyme binding site #248.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
KW restenosis; ss.
XX
OS Mammalia.
XX
FN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-O110954.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX

DR WPI: 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 PS Disclosure: Page 66; 109pp; English.
 XX
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX
 SO Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;

Query Match 44.8%; Score 13; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 aattacagagtt 24
 |||||
 DB 7 aattacagagtt 19

RESULT 12
 AAA83774
 ID AAA83774 standard; DNA: 19 BP.
 AC AAA83774;
 DT 04-DEC-2000 (first entry)
 XX cdk-we-hu ribozyme binding site #249.
 DE
 XX
 KW Ribozyme: hairpin; hammerhead; gene therapy; vasotropic;
 KM restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI: 2000-412314/35.
 XX
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 PS Disclosure: Page 66; 109pp; English.
 XX
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX

SO Sequence 19 BP; 7 A; 3 C; 4 G; 5 T; 0 other;

Query Match 44.8%; Score 13; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 aattacagagtt 24
 |||||
 DB 6 aattacagagtt 18

RESULT 13
 AAA83775
 ID AAA83775 standard; DNA: 19 BP.
 AC AAA83775;
 DT 04-DEC-2000 (first entry)
 XX cdk-we-hu ribozyme binding site #250.
 DE
 XX
 KW Ribozyme: hairpin; hammerhead; gene therapy; vasotropic;
 KM restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US28772.
 XX
 PR 04-DEC-1998; 98US-0110954.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI: 2000-412314/35.
 XX
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1 -
 PS Disclosure: Page 66; 109pp; English.
 XX
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX
 SO Sequence 19 BP; 7 A; 3 C; 4 G; 5 T; 0 other;
 Query Match 44.8%; Score 13; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 aattacagagtt 24
 |||||
 DB 5 aattacagagtt 17
 RESULT 14
 AAH58935
 ID AAH58935 standard; DNA: 19 BP.
 AC AAH58935;

XX 10-SEP-2001 (first entry)
 XX Cdk-we-hu ribozyme binding site SEQ ID NO:1359.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antitumor; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX 26-OCT-1999; 99US-0161532.
 XX (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 XX Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX Example 1; Page 170; 408pp; English.
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, vulnary, antiseborrheic, antidiabetic, antitumor,
 CC ophthalmological, cytostatic, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;

Query Match 44.8%; Score 13; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 aattacagagttt 24
 Db 7 aattacagagttt 19
 |||||

RESULT 15

AAH58936
 ID AAH58936 standard; DNA; 19 BP.
 XX AC AAH58936;
 XX 10-SEP-2001 (first entry)
 XX Cdk-we-hu ribozyme binding site SEQ ID NO:1360.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antitumor; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US29500.
 XX 26-OCT-1999; 99US-0161532.
 XX (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 XX Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX Example 1; Page 170; 408pp; English.
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antitumor,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX Sequence 19 BP; 7 A; 3 C; 4 G; 5 T; 0 other;

Query Match 44.8%; Score 13; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 aattacagagttt 24
 |||||

Fri Jun 21 14:52:03 2002

Db 6 aattacagagtt 18

Search completed: June 20, 2002, 23:10:05
Job time: 30170 sec

us-09-509-234c-1_1300_1328.primer.rng

Fri Jun 21 14:52:04 2002

c 977 9.4 32.4 37 4 US-09-153-310-25
 c 978 9.4 32.4 38 1 US-08-283-067-9
 c 979 9.4 32.4 38 1 US-08-283-067-38
 c 980 9.4 32.4 38 1 US-08-283-067-47
 c 981 9.4 32.4 38 1 US-08-428-370A-1
 c 982 9.4 32.4 38 1 US-08-428-370A-1
 c 983 9.4 32.4 38 2 US-08-600-764-1
 c 984 9.4 32.4 38 3 US-08-721-458B-29
 c 985 9.4 32.4 38 4 US-09-476-299-48
 c 986 9.4 32.4 38 4 US-09-609-154-48
 c 987 9.4 32.4 39 1 US-08-349-867-1
 c 988 9.4 32.4 39 1 US-08-239-476-1
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 c 990 9.4 32.4 39 1 US-07-854-603-5
 c 991 9.4 32.4 39 1 US-08-598-305A-1
 c 992 9.4 32.4 39 2 US-08-639-923A-1
 c 993 9.4 32.4 39 2 US-08-732-495-1
 c 994 9.4 32.4 39 3 US-08-109-037-8
 c 995 9.4 32.4 39 3 US-08-109-037-37
 c 996 9.4 32.4 39 3 US-08-109-037-38
 c 997 9.4 32.4 39 3 US-08-109-037-39
 c 998 9.4 32.4 39 4 US-09-358-036-21
 c 999 9.4 32.4 39 4 US-09-358-036-68
 c1000 9.4 32.4 40 2 US-08-628-422-8

ALIGNMENTS

RESULT 1
 US-08-874-102-23/c
 ; Sequence 23, Application US/08874102
 ; Patent No. 6309644
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramaswamy Chandrashekar
 ; APPLICANT: Kapil Mehta
 ; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
 ; TITLE OF INVENTION: AND USES THEREOF
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 12-JUN-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Verser, Carol Talkington
 ; REGISTRATION NUMBER: 37,459
 ; REFERENCE/DOCKET NUMBER: HW-2-C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 970/493-7272
 ; TELEFAX: 970/484-9505
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 nucleotides
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: primer
 ; US-08-874-102-23

Query Match 48.3%; Score 14; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 atgaattacaga 21
 |||
 Db 33 ATGAATTACAGA 20
 |||
 RESULT 2
 US-08-874-102-24
 ; Sequence 24, Application US/08874102
 ; Patent No. 6309644
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramaswamy Chandrashekar
 ; APPLICANT: Kapil Mehta
 ; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
 ; TITLE OF INVENTION: AND USES THEREOF
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 12-JUN-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Verser, Carol Talkington
 ; REGISTRATION NUMBER: 37,459
 ; REFERENCE/DOCKET NUMBER: HW-2-C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 970/493-7272
 ; TELEFAX: 970/484-9505
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 nucleotides
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: primer
 ; US-08-874-102-24
 Query Match 48.3%; Score 14; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 atgaattacaga 21
 |||
 Db 13 ATGAATTACAGA 26
 |||
 RESULT 3
 US-08-874-102-51
 ; Sequence 51, Application US/08874102
 ; Patent No. 6309644
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramaswamy Chandrashekar
 ; APPLICANT: Kapil Mehta
 ; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
 ; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
 ; TITLE OF INVENTION: AND USES THEREOF

;; TITLE OF INVENTION: AND USES THEREOF
;; NUMBER OF SEQUENCES: 59
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carol Talkington Verser, Ph.D.
;; ADDRESSEE: Heska Corporation
;; STREET: 1825 Sharp Point Drive
;; CITY: Fort Collins
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80525
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: WordPerfect for Windows, Version 7.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/874,102
;; FILING DATE: 12-JUN-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: HW-2-C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;; INFORMATION FOR SEQ ID NO: 51:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 45 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..45
;; US-08-874-102-51

Query Match 48.3%; Score 14; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
Db 13 ATGAATTACAGA 26

RESULT 4
US-08-874-102-53/C
Sequence 53, Application US/08874102
Patent No. 6309644
GENERAL INFORMATION:
APPLICANT: Ramaswamy Chandrasekar
TITLE OF INVENTION: PARASITIC NEMATODE TRANSGUTAMINASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/874,102
;; FILING DATE: 12-JUN-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: HW-2-C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 45 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-08-874-102-53

Query Match 48.3%; Score 14; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 atgaattacaga 21
Db 33 ATGAATTACAGA 20

RESULT 5
US-08-887-480-95/C
Sequence 95, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melys, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer JB614"
US-08-887-480-95

us-09-509-234c-1_1300_1328.primers.rni

Fri Jun 21 14:52:04 2002

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; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,346
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GIESSEY, JOANNE M
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19642Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3046
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-803-346-34

Query Match 44.1%; Score 12.8; DB 4; Length 28;
Best Local Similarity 87.5%; Pred. No. 8e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

QY 11 aaattacagagtaa 26
    ||| |||| |||||
Db 6 AAATTACAGAGTTAA 21

RESULT 8
US-09-117-860-56
; Sequence 56, Application US/09117860A
; Patent No. 6338955
; GENERAL INFORMATION:
; APPLICANT: OGURI, Suguru
; APPLICANT: MINOWA, Mari
; APPLICANT: YOSHIDA, Aruto
; APPLICANT: TANIGUCHI, Naoyuki
; APPLICANT: TAKEUCHI, Makoto
; TITLE OF INVENTION: NOVEL 1-4 N-ACETYLGLUCOSAMINYLTTRANSFERASE AND GENE
; FILE REFERENCE: 081356/0119
; CURRENT APPLICATION NUMBER: US/09/117,860A
; CURRENT FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: WO PCT/JP97/04546
; EARLIER FILING DATE: 1997-12-10
; EARLIER APPLICATION NUMBER: JP 161462/1997
; EARLIER FILING DATE: 1997-06-18
; EARLIER APPLICATION NUMBER: JP 332411/1996
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56
; LENGTH: 32

Query Match 44.1%; Score 12.8; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 8e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 11 aaattacagagtaa 26
    ||||| ||||| |||
Db 17 AAATTACAGAGTTA 2

RESULT 7
US-08-905-314A-15
; Sequence 34, Application US/08803346
; Patent No. 6281346
; GENERAL INFORMATION:
; APPLICANT: HESS, JOHN W.
; APPLICANT: CASKEY, C. THOMAS
; APPLICANT: LIU, QINGYUN
; APPLICANT: PHILLIPS, MICHAEL SEAN
; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES

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us-09-509-234c-1_1300_1328.primr.nrl

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-117-860-56

Query Match 43.4%; Score 12.6; DB 4; Length 32;
Best Local Similarity 78.9%; Pred. No. 1e+03; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4

OY 8 atgaattacagagttaa 26
||| ||| | ||| |||
DB 3 atgattataagagttaa 21

RESULT 9
US-08-171-389-206/c
Sequence 206, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA: US 08/081,070
APPLICATION NUMBER: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE

INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene
US-08-171-389-206

Query Match 43.4%; Score 12.6; DB 1; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4

OY 8 atgaattacagagttaa 26
||| ||| | ||| |||
DB 32 ATGCAATTACTACTGTTAA 14

RESULT 10
US-08-123-936-206/c
Sequence 206, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE
INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene
US-08-123-936-206

Query Match 43.4%; Score 12.6; DB 1; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4

OY 8 atgaattacagagttaa 26
||| ||| | ||| |||

```

Db      32  ATGCAATTTACTGTTAA 14

RESULT 11
US-08-475-228A-206/c
; Sequence 206, Application US/08475228A
; Patent No. 5869241
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,228A
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human Interleukin-2 (IL-2) gene
US-08-475-228A-206

Query Match      43.4%; Score 12.6; DB 2; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      8  atgaattacagagttaa 26
      ||| ||||| |||||
Db      32  ATGCAATTTACTGTTAA 14

RESULT 12
US-08-482-080A-206/c
; Sequence 206, Application US/08482080A
; Patent No. 6010849
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,080A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,389
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene
US-08-482-080A-206

Query Match      43.4%; Score 12.6; DB 3; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      8  atgaattacagagttaa 26
      ||| ||||| |||||
Db      32  ATGCAATTTACTGTTAA 14

RESULT 13
PCT-US93-12388-206/c

```

Sequence 206, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fadian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human Interleukin-2 (IL-2) gene
PCT-US93-12388-206

Query Match 43.4%; Score 12.6; DB 5; Length 46;
Best Local Similarity 78.9%; Pred. No. 1e+03; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||| ||||| |||||
Db 32 AGCAATTACTGTAA 14

RESULT 14
US-08-832-883-97/c
Sequence 97, Application US/08832883
Patent No. 5807681
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P. C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA

ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
TELEFAX: (215) 568-8383
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: other nucleic acid
US-08-832-883-97

Query Match 42.8%; Score 12.4; DB 1; Length 22;
Best Local Similarity 92.9%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 attacagagttaa 26
| ||||| |||||
Db 20 AGTACAGAGTTAA 7

RESULT 15
US-08-832-877-97/c
Sequence 97, Application US/08832877
Patent No. 5840506
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P. C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
TELEFAX: (215) 568-8383
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

us-09-509-234c-l_1300_1328.primer.rni

Fri Jun 21 14:52:04 2002

TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-932-877-97

Query Match 42.8%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. NO. 1.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 attacagaggttaa 26
DB 20 AGTTACAGAGTTAA 7

Search completed: June 20, 2002, 23:43:31
Job time: 5191 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 23:05:46 ; Search time 2574.69 Seconds
(Without alignments)
152.023 Million cell updates/sec

Title: US-09-509-234c-1_COPY_1300_1328

Perfect score: 29

Sequence: 1 nnnnnnataaattacagagtgtaann 29

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues 88996

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 15
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: em_estda:*
2: em_estlun:*
3: em_estlin:*
4: em_estlun:*
5: em_estlun:*
6: em_estlun:*
7: em_estlun:*
8: em_estlun:*
9: gb_estl:*
10: gb_estl:*
11: gb_estl:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	45.0	45	12	A2853600 2M0156E23
2	13.2	45.5	46	12	A2801977 2M0060K08
3	12.8	44.1	49	9	AA154640 md44g11.r
4	12.6	43.4	45	10	BE369365 601220740
5	12.6	43.4	49	10	B045819 B045819
6	12.2	42.1	41	12	A2462621 1M0269C07
7	12.2	42.1	48	10	B052421 B052421
8	12.2	42.1	49	10	B034980 B034980
9	11.8	40.7	34	12	A2764028 1M0559G13
10	11.6	40.0	29	12	A2345539 1M0080P03
11	11.6	40.0	33	10	DI87718
12	11.6	40.0	36	12	TA928110
13	11.6	40.0	37	10	B014578
14	11.6	40.0	37	10	C00973
15	11.6	40.0	37	10	DI9990
16	11.6	40.0	40	9	AJ237274
17	11.6	40.0	50	9	AU105018
18	11.6	40.0	50	9	AU105049
19	11.6	40.0	50	9	AU105067
20	11.6	40.0	50	9	AU105078
21	11.6	40.0	50	9	AU105081
22	11.4	39.3	34	12	BH146174
23	11.4	39.3	35	12	A2761537
24	11.4	39.3	41	9	AM335152
25	11.4	39.3	42	10	D21033
26	11.4	39.3	44	12	A2341932
27	11.2	38.6	27	12	A2798977
28	11.2	38.6	21	12	A2433270
29	11.2	38.6	30	12	A2628643
30	11.2	38.6	33	10	B0605523
31	11.2	38.6	37	10	C00973
32	11.2	38.6	40	10	D21037
33	11.2	38.6	40	12	A2769030
34	11.2	38.6	42	12	A2442090
35	11.2	38.6	47	12	A2628175
36	11.2	38.6	48	12	A2492954
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39	11.2	38.6	50	9	AU104949
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41	11.2	37.9	35	12	A2781345
42	11.2	37.9	36	12	A236982
43	11.2	37.9	37	9	A1574120
44	11.2	37.9	37	12	A2338392
45	11.2	37.9	41	10	D11997
46	11.2	37.9	42	9	AU060450
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48	11.2	37.9	45	12	BH627736
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57	10.8	37.2	22	12	A2991140
58	10.8	37.2	23	12	A2645569
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66	10.8	37.2	49	12	A2793862
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76	10.6	36.6	38	12	A2859079
77	10.6	36.6	39	12	A2949929
78	10.6	36.6	39	12	A2945552
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81	10.6	36.6	41	10	T17577
82	10.6	36.6	41	12	A2333189
83	10.6	36.6	42	12	A2972457
84	10.6	36.6	45	12	A2592674
85	10.6	36.6	46	12	A2332059
86	10.6	36.6	49	9	A1931428
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88	10.6	36.6	50	9	AU103031
89	10.6	36.6	50	9	AU103850
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91	10.4	35.9	31	9	AU009970	AU009970	10	34.5	43	12	TA53C02Q	AL456734 T. brucei
92	10.4	35.9	31	9	AU009989	AU009989	10	34.5	45	12	AZ666608	IM0348D23
93	10.4	35.9	34	12	AZ466488	AZ466488	10	34.5	46	10	BE914990	B01668031
94	10.4	35.9	34	12	AZ796078	2M0517F03	10	34.5	47	10	D20660	HUMGS01636
95	10.4	35.9	35	12	TA241A10P	AL481623 T. brucei	10	34.5	47	12	AZ490582	IM0323F12
96	10.4	35.9	36	12	AZ317022	AZ317022	10	34.5	48	10	D18211	MUGS00482
97	10.4	35.9	37	9	AA742638	ny91a06.s	10	34.5	48	12	AZ331576	IM0059005
98	10.4	35.9	42	9	AA610176	ny91a06.s	10	34.5	49	9	AI303303	u167c01.y
99	10.4	35.9	43	9	AA921819	vm20d12.s	10	34.5	49	9	AZ228955	nc14a06.r
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102	10.4	35.9	44	12	TA79G02Q	AL461510 T. brucei	10	34.5	49	9	AV245974	AV245974
103	10.4	35.9	45	12	AZ810685	2M0076G34	10	34.5	50	9	AU103081	AU103081
104	10.4	35.9	47	9	AV858479	AV858479	10	34.5	50	9	AU103082	AU103082
105	10.2	35.2	23	12	AZ873619	2M0187M21	10	34.5	50	9	AU104173	AU104173
106	10.2	35.2	25	12	AZ655691	1M0530K16	10	34.5	50	9	AU105011	AU105011
107	10.2	35.2	26	12	AZ303927	1M0003H19	10	34.5	50	9	AU105012	AU105012
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109	10.2	35.2	31	12	AZ371109	1M0122D104	10	34.5	50	9	AU105014	AU105014
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111	10.2	35.2	33	12	AZ445749	1M0241P15	10	34.5	50	9	AU105019	AU105019
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115	10.2	35.2	37	9	AI327021	mj94f07.x	10	34.5	50	9	AU105024	AU105024
116	10.2	35.2	38	12	AZ797817	2M0054E18	10	34.5	50	9	AU105025	AU105025
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118	10.2	35.2	40	12	AZ849854	2M0151P23	10	34.5	50	9	AU105028	AU105028
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120	10.2	35.2	43	12	AZ813036	2M0080D10	10	34.5	50	9	AU105031	AU105031
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123	10.2	35.2	45	12	AZ806160	2M0068I02	10	34.5	50	9	AU105035	AU105035
124	10.2	35.2	47	10	BF084126	BJ084126	10	34.5	50	9	AU105036	AU105036
125	10.2	35.2	48	10	BF159807	601767061	10	34.5	50	9	AU105037	AU105037
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127	10.2	35.2	49	9	AI652389	wb20e07.x	10	34.5	50	9	AU105039	AU105039
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132	10.2	35.2	50	9	AU104948	AU104948	10	34.5	50	9	AU105044	AU105044
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134	10.2	35.2	50	12	AZ834813	2M0117010	10	34.5	50	9	AU105048	AU105048
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137	10.2	35.2	52	12	AZ498180	1M0335A24	10	34.5	50	9	AU105051	AU105051
138	10.2	35.2	52	12	AZ371108	1M0122I03	10	34.5	50	9	AU105052	AU105052
139	10.2	35.2	52	12	TA109B05P	TA109B05P	10	34.5	50	9	AU105053	AU105053
140	10.2	35.2	52	12	AZ438866	1M0229K10	10	34.5	50	9	AU105054	AU105054
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142	10.2	35.2	53	9	AU008904	AU008904	10	34.5	50	9	AU105071	AU105071
143	10.2	35.2	53	9	AU008906	AU008906	10	34.5	50	9	AU105072	AU105072
144	10.2	35.2	53	12	AZ488329	1M0318I05	10	34.5	50	9	AU105076	AU105076
145	10.2	35.2	53	12	AZ657897	1M0534F19	10	34.5	50	9	AU105077	AU105077
146	10.2	35.2	53	12	TA254H07P	AL482475 T. brucei	10	34.5	50	9	AU105080	AU105080
147	10.2	35.2	53	12	AZ438586	1M0228E15	10	34.5	50	9	AU105083	AU105083
148	10.2	35.2	53	12	AU053071	AU053071	10	34.5	50	9	AU105084	AU105084
149	10.2	35.2	53	12	AZ310803	1M0025L21	10	34.5	50	9	AU105085	AU105085
150	10.2	35.2	53	12	AZ463024	1M0271C09	10	34.5	50	9	AU105087	AU105087
151	10.2	35.2	53	12	TA164B05Q	AL473134 T. brucei	10	34.5	50	9	AU105088	AU105088
152	10.2	35.2	53	12	AZ404740	1M0173D10	10	34.5	50	9	AU105089	AU105089
153	10.2	35.2	53	12	C21579	HUMGS001038	10	34.5	50	9	AU105090	AU105090
154	10.2	35.2	53	12	AZ799964	2M0057B18	10	34.5	50	9	AU105091	AU105091
155	10.2	35.2	53	12	AZ82514	2M0022N20	10	34.5	50	9	AU105092	AU105092
156	10.2	35.2	53	12	AU011117	AU011117	10	34.5	50	9	AU105093	AU105093
157	10.2	35.2	53	12	TA174C05Q	AL474511 T. brucei	10	34.5	50	9	AU105094	AU105094
158	10.2	35.2	53	12	TA348G01Q	AL496200 T. brucei	10	34.5	50	9	AU106291	AU106291
159	10.2	35.2	53	12	AA179309	zp45c09.s	10	34.5	50	9	AA566984	AA566984
160	10.2	35.2	53	9	AA14055	vc58d05.s	10	34.5	50	10	BJ066224	BJ066224
161	10.2	35.2	53	10	BI147462	602914038	10	34.5	50	12	AZ499993	AZ499993
162	10.2	35.2	53	10	D20671	HUMGS01647	10	34.5	50	12	TA120E02Q	TA120E02Q
163	10.2	35.2	53	12	AZ793113	2M0046P06	10	34.5	50	12	AZ862758	AZ862758

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238	9.8	33.8	23	12	A2802457	A2802457 2M0061C23	c 311	9.6	33.1	37	9	A2948700	A2948700 0044509.s
239	9.8	33.8	25	12	A2627851	A2627851 1M0476B04	312	9.6	33.1	37	9	A1636802	A1636802 t556c09.x
240	9.8	33.8	25	12	A2789794	A2789794 2M0037J21	313	9.6	33.1	37	12	A2503091	A2503091 1M0542P12
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242	9.8	33.8	28	12	A2478220	A2478220 1M0298R08	315	9.6	33.1	38	12	A2363970	A2363970 1M0109M19
243	9.8	33.8	30	12	A2346661	A2346661 1M0082B04	c 316	9.6	33.1	38	12	A2591868	A2591868 1M0402M17
244	9.8	33.8	30	12	A2400595	A2400595 1M0166P19	c 317	9.6	33.1	38	12	A2759828	A2759828 1M0552K22
245	9.8	33.8	30	12	A2838298	A2838298 2M0133L23	c 318	9.6	33.1	38	12	A2806560	A2806560 2M0068M11
246	9.8	33.8	31	9	A1126669	A1126669 qc52c04.x	c 319	9.6	33.1	38	12	A2837547	A2837547 2M0132E20
247	9.8	33.8	32	10	C20893	C20893 HDMS000496	c 320	9.6	33.1	39	9	AV851787	AV851787 AV851787
248	9.8	33.8	32	12	TA113A05P	TA113A05P T. bruce1	321	9.6	33.1	40	9	AA93635	AA93635 o165d11.s
249	9.8	33.8	33	10	D25860	D25860 HDMS04237	c 322	9.6	33.1	40	9	A1208300	A1208300 qc59n12.x
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251	9.8	33.8	34	9	AU006691	AU006691 AU006691	c 324	9.6	33.1	40	10	AA99367	AA99367 v189p06.r
252	9.8	33.8	34	12	A2778432	A2778432 2M0013A15	c 325	9.6	33.1	40	12	D18705	D18705 HDMS001767
253	9.8	33.8	35	9	AU116316	AU116316 AU116316	c 326	9.6	33.1	40	12	A2300900	A2300900 EP(X)1358
254	9.8	33.8	35	12	A2339968	A2339968 1M0071M08	c 327	9.6	33.1	40	12	A2595949	A2595949 1M0408I24
255	9.8	33.8	36	9	A1448911	A1448911 ms50912.x	c 328	9.6	33.1	42	9	A2664762	A2664762 1M0545P18
256	9.8	33.8	36	9	AV847228	AV847228 AV847228	c 329	9.6	33.1	42	9	AA455805	AA455805 2D2 Neuro
257	9.8	33.8	36	12	A2477016	A2477016 1M0296I13	c 330	9.6	33.1	43	9	A1749549	A1749549 at30d05.x
258	9.8	33.8	36	12	A2623431	A2623431 1M0461I09	c 331	9.6	33.1	43	10	B616319	B616319 602644559
259	9.8	33.8	37	9	A1314676	A1314676 u127d02.x	c 332	9.6	33.1	43	10	C21084	C21084 HDMS000259
260	9.8	33.8	37	10	C21093	C21093 HDMS000260	c 333	9.6	33.1	43	10	BE571395	BE571395 601330251
261	9.8	33.8	38	10	D19987	D19987 HDMS00954	c 334	9.6	33.1	43	12	A2786639	A2786639 2M0032F14
262	9.8	33.8	39	10	B049570	B049570 B049570	c 335	9.6	33.1	44	12	A2322603	A2322603 1M0043M21
263	9.8	33.8	39	10	B081937	B081937 B081937	c 336	9.6	33.1	44	12	A2778806	A2778806 2M0014B19
264	9.8	33.8	39	10	C01981	C01981 HDMS000399	c 337	9.6	33.1	44	12	A2860516	A2860516 2M0166T04
265	9.8	33.8	39	10	D12202	D12202 HDMS000535	c 338	9.6	33.1	44	12	A2695920	A2695920 2M0242M15
266	9.8	33.8	39	10	D18708	D18708 HDMS01770	c 339	9.6	33.1	45	12	A2760031	A2760031 1M0553M20
267	9.8	33.8	39	10	D19134	D19134 HDMS001350	c 340	9.6	33.1	45	12	A2769369	A2769369 1M0569023
268	9.8	33.8	40	9	AA288878	AA288878 m143h01.r	c 341	9.6	33.1	46	9	A1805932	A1805932 t62903.x
269	9.8	33.8	40	10	C00336	C00336 HDMS000238	c 342	9.6	33.1	46	10	N54785	N54785 yv31a05.s1
270	9.8	33.8	43	10	R27800	R27800 yb5ea01.s1	c 343	9.6	33.1	46	12	A2319339	A2319339 1M0018G19
271	9.8	33.8	43	12	A2769954	A2769954 1M0571E11	c 344	9.6	33.1	46	12	A2445552	A2445552 1M0241M18
272	9.8	33.8	44	10	C21087	C21087 HDMS000260	c 345	9.6	33.1	46	12	A2487823	A2487823 1M0317B17
273	9.8	33.8	45	9	AA091874	AA091874 ft0146.se	c 346	9.6	33.1	46	12	A2778586	A2778586 2M0013N16
274	9.8	33.8	45	12	A2345662	A2345662 1M0080N21	c 347	9.6	33.1	47	9	AA087264	AA087264 mo12110.r
275	9.8	33.8	45	12	A2424118	A2424118 1M0203J05	c 348	9.6	33.1	47	10	D19125	D19125 HDMS001339
276	9.8	33.8	45	12	A2782306	A2782306 2M0022A05	c 349	9.6	33.1	47	12	A2596995	A2596995 1M0410A08
277	9.8	33.8	45	12	A2864702	A2864702 2M0174K23	c 350	9.6	33.1	47	12	A2632265	A2632265 1M0488R23
278	9.8	33.8	46	9	AA645258	AA645258 vs80c07.r	c 351	9.6	33.1	47	12	A2662467	A2662467 1M0541P03
279	9.8	33.8	46	10	C20885	C20885 HDMS000495	c 352	9.6	33.1	47	12	A2769254	A2769254 1M0569B16
280	9.8	33.8	47	12	A2474384	A2474384 1M0290O24	c 353	9.6	33.1	47	12	TA290H07P	TA290H07P
281	9.8	33.8	48	10	H00563	H00563 y12aell.s1	c 354	9.6	33.1	48	10	D19123	D19123 HDMS001337
282	9.8	33.8	48	12	A2307096	A2307096 1M0008O19	c 355	9.6	33.1	48	12	A2843479	A2843479 2M0142C23
283	9.8	33.8	48	12	A2307096	A2307096 1M0127B02	c 356	9.6	33.1	48	12	AA675211	AA675211 v165b09.s
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285	9.8	33.8	49	9	AA500776	AA500776 vq01b11.r	c 358	9.6	33.1	49	9	A1609521	A1609521 tw90f12.x
286	9.8	33.8	49	10	H10690	H10690 ym07h01.r1	c 359	9.6	33.1	49	9	AV836810	AV836810 AV836810
287	9.8	33.8	49	12	A2331612	A2331612 1M0059I10	c 360	9.6	33.1	49	10	BG364043	BG364043 dc73h10.Y
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290	9.6	33.1	21	12	A2345459	A2345459 1M0080K12	c 363	9.6	33.1	49	10	H39410	H39410 DRL02 IPN84
291	9.6	33.1	21	12	A2345459	A2345459 1M0080K12	c 364	9.6	33.1	49	10	H39410	H39410 DRL02 IPN84
292	9.6	33.1	22	12	A2621574	A2621574 1M0454C24	c 365	9.6	33.1	49	10	BF033160	BF033160 601454591
293	9.6	33.1	22	12	A2387817	A2387817 1M0147B24	c 366	9.6	33.1	49	12	A2809636	A2809636 2M0073A17
294	9.6	33.1	23	12	A2387817	A2387817 1M0147B24	c 367	9.6	33.1	50	9	AA180898	AA180898 zpa1907.s
295	9.6	33.1	24	12	A2464973	A2464973 1M0274D08	c 368	9.6	33.1	50	9	AU103568	AU103568 AU103568
296	9.6	33.1	25	9	A1761999	A1761999 wh50g09.x	c 369	9.6	33.1	50	9	AU104887	AU104887 AU104887
297	9.6	33.1	25	12	A2817197	A2817197 2M0086H19	c 370	9.6	33.1	50	9	AU105073	AU105073 AU105073
298	9.6	33.1	28	12	A2424470	A2424470 1M0204A07	c 371	9.6	33.1	50	9	AU105956	AU105956 AU105956
299	9.6	33.1	29	12	A2582213	A2582213 1M0374D07	c 372	9.6	33.1	50	9	AU106905	AU106905 AU106905
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301	9.6	33.1	31	9	AA591377	AA591377 v15a11.r	c 374	9.6	33.1	50	10	BM069631	BM069631 l690a09.y
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304	9.6	33.1	33	9	AU014077	AU014077 AU014077	c 377	9.6	33.1	50	12	A2921856	A2921856 HRC02H06
305	9.6	33.1	34	9	AA929809	AA929809 vy75d06.r	c 378	9.6	33.1	50	12	TA288H06Q	TA288H06Q
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307	9.6	33.1	34	12	A2590006	A2590006 1M0398B23	c 380	9.6	33.1	50	12	A2663184	A2663184 1M0542L07
308	9.6	33.1	35	9	AU009945	AU009945 AU009945	c 381	9.6	33.1	19	12	A2798955	A2798955 2M0056K01
309	9.6	33.1	36	12	A2339979	A2339979 1M0071O08	c 382	9.6	33.1	20	10	D45831	D45831 HDMS003052

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385	9.4	32.4	21	12	AZ811635	2M0077B21	C 458	9.4	32.4	43	12	BH627531	1007094C0
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389	9.4	32.4	24	10	AZ423817	1M0203P19	C 462	9.4	32.4	43	12	BH632235	1007094C0
390	9.4	32.4	25	12	AZ641910	1M0504N09	C 463	9.4	32.4	44	10	BH782524	1007094C0
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392	9.4	32.4	26	12	AZ783032	2M0024F21	C 465	9.4	32.4	44	10	BH782524	1007094C0
393	9.4	32.4	26	12	AZ809397	2M0073E22	C 466	9.4	32.4	44	10	BH782524	1007094C0
394	9.4	32.4	28	12	AZ603349	1M0422H15	C 467	9.4	32.4	44	12	AZ592662	1M0403C15
395	9.4	32.4	28	12	AZ641858	1M0504D11	C 468	9.4	32.4	44	12	AZ779656	2M0016B22
396	9.4	32.4	29	12	AZ853131	2M0156H11	C 469	9.4	32.4	44	12	AZ779656	2M0016B22
397	9.4	32.4	29	12	AZ853131	2M0156H11	C 470	9.4	32.4	44	12	BH621197	1007117E0
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399	9.4	32.4	31	9	AA757938	vk24h02.s	C 472	9.4	32.4	44	12	BH621197	1007117E0
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409	9.4	32.4	33	12	TA313005P	bruce1	C 482	9.4	32.4	44	12	BH621197	1007117E0
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443	9.4	32.4	42	9	AU060450	AU060450	C 516	9.4	32.4	44	12	BH621197	1007117E0
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448	9.4	32.4	42	12	BH630977	1007095G1	C 521	9.4	32.4	44	12	BH621197	1007117E0
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474	9.4	32.4	43	12	BH622585	1007090C0	C 547	9.4	32.4	44	12	BH621197	1007117E0
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C 531	9.4	32.4	50	9	AU103705	AU103705 AU103705	C 604	9.2	31.7	39	12	AZ809941	AZ809941 2M0074L11
C 532	9.4	32.4	50	9	AU107045	AU107045 AU107045	C 605	9.2	31.7	40	12	AZ781550	AZ781550 2M0025H06
C 533	9.4	32.4	50	10	AA422502	AA422502 v14f06.s	C 606	9.2	31.7	40	12	AZ804734	AZ804734 2M0065F11
C 534	9.4	32.4	50	10	BG071172	BG071172 H3095E07-	C 607	9.2	31.7	40	12	AZ809875	AZ809875 2M0074N02
C 535	9.4	32.4	50	10	BG147876	BG147876 w13a07.y	C 608	9.2	31.7	40	12	AZ810561	AZ810561 2M0076F10
C 536	9.4	32.4	50	10	BML83051	BML83051 fw29g09.y	C 609	9.2	31.7	40	12	AZ810561	AZ810561 2M0076F10
C 537	9.4	32.4	50	10	BE887296	BE887296 601510J12	C 610	9.2	31.7	41	12	AZ860963	AZ860963 1M0181F22
C 538	9.4	32.4	50	12	AZ424190	AZ424190 1M0203J12	C 611	9.2	31.7	41	12	AA680963	AA680963 1M0213G16
C 539	9.4	32.4	50	12	AZ460815	AZ460815 1M0266A24	C 612	9.2	31.7	42	10	C21089	C21089 HDG5000260
C 540	9.4	32.4	50	12	AZ769249	AZ769249 1M0569P12	C 613	9.2	31.7	42	12	AZ822505	AZ822505 2M0095F15
C 541	9.4	32.4	50	12	AZ805722	AZ805722 2M0067H14	C 614	9.2	31.7	42	12	BH023748	BH023748 BG01746-5
C 542	9.4	32.4	50	12	AZ860602	AZ860602 2M0066K09	C 615	9.2	31.7	42	12	TA61E040	TA61E040 T. bruce1
C 543	9.4	32.4	50	12	BH631106	BH631106 1007096H0	C 616	9.2	31.7	42	12	AA846206	AA846206 a183a12.s
C 544	9.4	32.4	50	12	AZ345537	AZ345537 1M0080P01	C 617	9.2	31.7	43	9	AJ237201	AJ237201 AJ237201
C 545	9.2	31.7	19	12	AZ973582	AZ973582 2M0247C20	C 618	9.2	31.7	43	10	H39896	H39896 yp02f02.81
C 546	9.2	31.7	19	12	AZ973582	AZ973582 1M0257K08	C 619	9.2	31.7	43	12	AA025688	AA025688 1(2)K060
C 547	9.2	31.7	20	12	AZ818725	AZ818725 2M0088K20	C 620	9.2	31.7	43	12	AZ333179	AZ333179 1M0062D08
C 548	9.2	31.7	22	12	TA82E070	TA82E070 T. bruce1	C 621	9.2	31.7	43	12	AZ778538	AZ778538 2M0013G11
C 549	9.2	31.7	22	12	DA5827	DA5827 HDG503047	C 622	9.2	31.7	44	10	D20693	D20693 HDG501645
C 550	9.2	31.7	23	10	DA5827	DA5827 HDG503047	C 623	9.2	31.7	44	12	AZ591404	AZ591404 1M0401C03
C 551	9.2	31.7	23	10	DA5827	DA5827 HDG503047	C 624	9.2	31.7	44	12	TA189C01P	TA189C01P T. bruce1
C 552	9.2	31.7	23	12	AZ346779	AZ346779 1M0082K08	C 625	9.2	31.7	45	9	AU007315	AU007315 AU007315
C 553	9.2	31.7	24	12	AZ332511	AZ332511 1M0061I02	C 626	9.2	31.7	45	10	BF141386	BF141386 601786322
C 554	9.2	31.7	24	12	AZ420211	AZ420211 1M0197C22	C 627	9.2	31.7	45	12	AZ835927	AZ835927 2M0130I22
C 555	9.2	31.7	25	9	AU013927	AU013927 AU013927	C 628	9.2	31.7	46	9	AA000884	AA000884 me76d05.r
C 556	9.2	31.7	25	10	D19152	D19152 MUGS03174	C 629	9.2	31.7	46	9	A1003237	A1003237 ant1h01.s
C 557	9.2	31.7	25	12	AZ595654	AZ595654 1M0408J22	C 630	9.2	31.7	46	10	W30168	W30168 mc2b02.r1
C 558	9.2	31.7	25	12	AZ810579	AZ810579 2M0076M08	C 631	9.2	31.7	46	12	AZ318180	AZ318180 1M0037J10
C 559	9.2	31.7	27	12	AZ57058	AZ57058 1M0260B13	C 632	9.2	31.7	46	12	AZ513160	AZ513160 1M00759H10
C 560	9.2	31.7	27	12	AZ806049	AZ806049 2M0067B20	C 633	9.2	31.7	47	12	LA6923	LA6923 SKMRP010.G
C 561	9.2	31.7	28	12	TA171H05Q	TA171H05Q T. bruce1	C 634	9.2	31.7	47	10	LA6923	LA6923 SKMRP010.G
C 562	9.2	31.7	28	12	AZ824349	AZ824349 2M0098G19	C 635	9.2	31.7	47	12	AZ597007	AZ597007 1M0410C12
C 563	9.2	31.7	29	12	AZ663777	AZ663777 1M0543P04	C 636	9.2	31.7	48	12	AZ31639	AZ31639 1M0059P07
C 564	9.2	31.7	29	12	AZ861809	AZ861809 2M0188C19	C 637	9.2	31.7	48	12	AZ458771	AZ458771 1M0263H10
C 565	9.2	31.7	29	12	TA330F03P	TA330F03P T. bruce1	C 638	9.2	31.7	48	12	AZ592310	AZ592310 1M0403D12
C 566	9.2	31.7	30	12	AZ458160	AZ458160 1M0262C06	C 639	9.2	31.7	49	9	AA760213	AA760213 vv7f01.f
C 567	9.2	31.7	30	12	AZ610538	AZ610538 1M0435E23	C 640	9.2	31.7	49	9	AA995234	AA995234 cut1a05.8
C 568	9.2	31.7	30	12	AZ658107	AZ658107 1M0534M12	C 641	9.2	31.7	49	9	AL653536	AL653536 AL653536
C 569	9.2	31.7	30	12	AZ863032	AZ863032 2M0031A13	C 642	9.2	31.7	49	9	AU006473	AU006473 AU006473
C 570	9.2	31.7	30	12	AV851547	AV851547 AV851547	C 643	9.2	31.7	49	10	BE916026	BE916026 601666326
C 571	9.2	31.7	32	9	AZ85437	AZ85437 1M0312B19	C 644	9.2	31.7	49	10	BF102833	BF102833 1M0008I23
C 572	9.2	31.7	32	12	AZ826689	AZ826689 2M0102D07	C 645	9.2	31.7	49	12	AZ458264	AZ458264 1M0262M10
C 573	9.2	31.7	32	12	TA251F03P	TA251F03P T. bruce1	C 646	9.2	31.7	49	12	AZ590749	AZ590749 1M0400D04
C 574	9.2	31.7	33	10	AV852712	AV852712 AV852712	C 647	9.2	31.7	49	12	TA119E020	TA119E020 T. bruce1
C 575	9.2	31.7	33	10	BE386592	BE386592 601273941	C 648	9.2	31.7	49	12	AA683896	AA683896 vt06e08.r
C 576	9.2	31.7	33	12	AZ387166	AZ387166 1M0146624	C 649	9.2	31.7	50	9	A1688854	A1688854 t143a04.x
C 577	9.2	31.7	33	12	AZ776083	AZ776083 2M0009P19	C 650	9.2	31.7	50	9	A1988040	A1988040 sc33a11.x
C 578	9.2	31.7	33	12	AZ776083	AZ776083 2M0009P19	C 651	9.2	31.7	50	9	AU102339	AU102339 AU102339
C 579	9.2	31.7	34	9	AA911163	AA911163 o136h05.s	C 652	9.2	31.7	50	9	AU103904	AU103904 AU103904
C 580	9.2	31.7	34	10	C21507	C21507 HDG5001050	C 653	9.2	31.7	50	9	AU103911	AU103911 AU103911
C 581	9.2	31.7	34	10	H26058	H26058 v152d09.r1	C 654	9.2	31.7	50	9	AV833364	AV833364 AV833364
C 582	9.2	31.7	34	12	AZ436112	AZ436112 1M0233F17	C 655	9.2	31.7	50	10	BI744280	BI744280 pb06g12.y
C 583	9.2	31.7	34	12	AZ655424	AZ655424 1M0530G16	C 656	9.2	31.7	50	12	AZ512131	AZ512131 1M0057C05
C 584	9.2	31.7	34	12	AZ785820	AZ785820 2M0030F05	C 657	9.2	31.7	50	12	AZ776841	AZ776841 2M0010P15
C 585	9.2	31.7	35	10	D19568	D19568 MUGS00973	C 658	9.2	31.7	50	12	TA346C05Q	TA346C05Q T. bruce1
C 586	9.2	31.7	35	12	AZ664413	AZ664413 1M0541D01	C 659	9.2	31.7	20	12	AZ421329	AZ421329 1M0420H13
C 587	9.2	31.7	35	12	AA811228	AA811228 2M0086P23	C 660	9.2	31.7	20	12	AZ465955	AZ465955 1M0276F14
C 588	9.2	31.7	37	9	AA811247	AA811247 op68a09.s	C 661	9.2	31.0	20	12	AZ409809	AZ409809 1M0481F08
C 589	9.2	31.7	37	9	A1823627	A1823627 v185e02.x	C 662	9.2	31.0	21	12	AZ602152	AZ602152 1M0481F08
C 590	9.2	31.7	37	9	AA832674	AA832674 AV832674	C 663	9.2	31.0	21	12	AZ838634	AZ838634 2M0134H22
C 591	9.2	31.7	37	9	AA832808	AA832808 SL1D3.AGS	C 664	9.2	31.0	21	12	AZ838634	AZ838634 2M0134H22
C 592	9.2	31.7	37	12	AZ597788	AZ597788 1M0411B21	C 665	9.2	31.0	24	12	AZ784850	AZ784850 1M0103E04
C 593	9.2	31.7	37	12	AZ769906	AZ769906 1M0571H06	C 666	9.2	31.0	24	12	AZ345506	AZ345506 2M0028G08
C 594	9.2	31.7	37	12	AZ775103	AZ775103 2M0007D08	C 667	9.2	31.0	25	12	AZ462644	AZ462644 1M0265M11
C 595	9.2	31.7	37	12	AZ784793	AZ784793 2M0028I01	C 668	9.2	31.0	25	12	AZ662625	AZ662625 1M0493P03
C 596	9.2	31.7	38	12	AZ453559	AZ453559 1M0255G03	C 669	9.2	31.0	26	12	AM333097	AM333097 517C3.AGS
C 597	9.2	31.7	38	12	AZ596174	AZ596174 1M0409I15	C 670	9.2	31.0	26	10	C53818	C53818 C53818 Yuj1
C 598	9.2	31.7	38	12	AZ855530	AZ855530 2M0159O14	C 671	9.2	31.0	27	12	TA310H02Q	TA310H02Q T. bruce1
C 599	9.2	31.7	39	9	AU011691	AU011691 AU011691	C 672	9.2	31.0	28	9	AA636083	AA636083 nt15b06.s
C 600	9.2	31.7	39	12	AZ321053	AZ321053 1M0041G24	C 673	9.2	31.0	28	9	AA194946	AA194946 u158f10.x
C 601	9.2	31.7	39	12	AZ417124	AZ417124 1M0192J07	C 674	9.2	31.0	28	9	AA194946	AA194946 u158f10.x

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C 821	8.8	30.3	27	12	TR274G11P	AL484616 T. brucei	C 894	8.8	30.3	42	9	AW257649	AW257649 SWWD256AU
C 822	8.8	30.3	28	10	C00220	C00220 HUMS000588	C 895	8.8	30.3	42	12	A2625578	A2625578 1M065X12
C 823	8.8	30.3	28	10	C00220	C00220 HUMS000588	C 896	8.8	30.3	42	12	A2780875	A2780875 2M018H07
C 824	8.8	30.3	28	12	A2656764	A2656764 1M0532R05	C 897	8.8	30.3	42	12	A2827115	A2827115 2M0103C21
C 825	8.8	30.3	28	12	A2839856	A2839856 2M0136T08	C 898	8.8	30.3	42	12	TA1C050	TA1C050 T. brucei
C 826	8.8	30.3	29	12	A2445583	A2445583 1M0336M14	C 899	8.8	30.3	43	9	AJ237201	AJ237201 AJ237201
C 827	8.8	30.3	29	12	A2514535	A2514535 1M0561H11	C 900	8.8	30.3	43	9	AU014497	AU014497 AU014497
C 828	8.8	30.3	30	12	AM698826	AM698826 r425 non-	C 901	8.8	30.3	43	10	T25548	T25548 HUMS00487
C 829	8.8	30.3	30	12	A2346834	A2346834 1M0082P15	C 902	8.8	30.3	43	10	T25548	T25548 EST00581 UN
C 830	8.8	30.3	31	9	AA980782	AA980782 ua45e10.r	C 903	8.8	30.3	43	12	A2370460	A2370460 1M0121D04
C 831	8.8	30.3	31	9	AA983748	AA983748 c165e02.s	C 904	8.8	30.3	43	12	A2807713	A2807713 2M0069G09
C 832	8.8	30.3	31	10	N22001	N22001 yw31d10.s1	C 905	8.8	30.3	43	12	A2830358	A2830358 2M0109M04
C 833	8.8	30.3	31	12	A2346724	A2346724 1M0082P05	C 906	8.8	30.3	43	12	A2861846	A2861846 2M0168L01
C 834	8.8	30.3	31	12	A2376156	A2376156 1M0129G22	C 907	8.8	30.3	44	10	D18694	D18694 T. brucei
C 835	8.8	30.3	31	12	A2437063	A2437063 1M0225C07	C 908	8.8	30.3	44	10	BE900863	BE900863 1M0563H15
C 836	8.8	30.3	31	12	A2441465	A2441465 1M0238B13	C 909	8.8	30.3	44	12	A2766302	A2766302 qx57b03.x
C 837	8.8	30.3	31	12	A2473655	A2473655 1M0289H09	C 910	8.8	30.3	44	12	A2766302	A2766302 qx57b03.x
C 838	8.8	30.3	32	12	A2352160	A2352160 1M0090P04	C 911	8.8	30.3	45	9	A1263295	A1263295 qx57b03.x
C 839	8.8	30.3	32	12	A2510121	A2510121 1M0354J74	C 912	8.8	30.3	45	9	AT844706	AT844706 AV844706
C 840	8.8	30.3	32	12	A2596075	A2596075 1M0409B08	C 913	8.8	30.3	45	10	BG669979	BG669979 DRMANB12
C 841	8.8	30.3	32	12	A2596075	A2596075 1M0514B09	C 914	8.8	30.3	45	10	A2513479	A2513479 1M0359P21
C 842	8.8	30.3	33	10	C01068	C01068 HUMS000771	C 915	8.8	30.3	45	12	A2586721	A2586721 2M0012J13
C 843	8.8	30.3	33	10	H55508	H55508 CHR220447 C	C 916	8.8	30.3	45	12	A2777920	A2777920 T. brucei
C 844	8.8	30.3	34	9	AA067695	AA067695 mms54d08.r	C 917	8.8	30.3	45	12	TA129F11P	TA129F11P T. brucei
C 845	8.8	30.3	34	9	A1130225	A1130225 SMOWL3CAN	C 918	8.8	30.3	46	12	TR82F07P	TR82F07P T. brucei
C 846	8.8	30.3	34	9	A1102906	A1102906 t295G03.x	C 919	8.8	30.3	46	9	AA959743	AA959743 1M0563H15
C 847	8.8	30.3	34	9	AV837777	AV837777 AV837777	C 920	8.8	30.3	46	9	AA959743	AA959743 1M0563H15
C 848	8.8	30.3	34	10	BU066450	BU066450 BU066450	C 921	8.8	30.3	46	10	BG971567	BG971567 60284M017
C 849	8.8	30.3	34	10	BU077560	BU077560 BU077560	C 922	8.8	30.3	46	12	A2470136	A2470136 1M0288M01
C 850	8.8	30.3	34	10	D20692	D20692 HUMG501668	C 923	8.8	30.3	46	12	AQ254727	AQ254727 EP(3)3520
C 851	8.8	30.3	34	10	T60701	T60701 yb69f02.s1	C 924	8.8	30.3	46	12	TR278A09P	TR278A09P T. brucei
C 852	8.8	30.3	34	12	A2333038	A2333038 1M0061H18	C 925	8.8	30.3	47	9	AV851743	AV851743 AV851743
C 853	8.8	30.3	34	12	A2761083	A2761083 1M0555A13	C 926	8.8	30.3	47	10	D19124	D19124 MUSG501338
C 854	8.8	30.3	36	12	AV847228	AV847228 AV847228	C 927	8.8	30.3	47	12	A23662217	A23662217 1M0707B16
C 855	8.8	30.3	36	12	A2331556	A2331556 1M0059E08	C 928	8.8	30.3	47	12	A2479400	A2479400 1M0500C04
C 856	8.8	30.3	36	12	A2334407	A2334407 1M0063H13	C 929	8.8	30.3	47	12	A2767816	A2767816 1M0567H24
C 857	8.8	30.3	36	12	A2339896	A2339896 1M0077M02	C 930	8.8	30.3	47	12	A2822668	A2822668 2M0096B09
C 858	8.8	30.3	36	12	A2454226	A2454226 1M0556P04	C 931	8.8	30.3	47	12	BM622724	BM622724 1007098A0
C 859	8.8	30.3	36	12	A2605771	A2605771 1M0427K13	C 932	8.8	30.3	47	12	TA129F11P	TA129F11P T. brucei
C 860	8.8	30.3	36	12	A2626864	A2626864 1M0467K21	C 933	8.8	30.3	48	12	A2835757	A2835757 2M0130P05
C 861	8.8	30.3	37	9	A1020959	A1020959 UD06H09.r	C 934	8.8	30.3	48	12	A2953988	A2953988 2M0219B01
C 862	8.8	30.3	37	9	A1332109	A1332109 fa94f02.y	C 935	8.8	30.3	49	9	AA727893	AA727893 v334C01.r
C 863	8.8	30.3	37	9	A1648795	A1648795 UK29D11.x	C 936	8.8	30.3	49	9	A15662828	A15662828 CH47811.s
C 864	8.8	30.3	37	9	AV833370	AV833370 AV833370	C 937	8.8	30.3	49	9	A1569150	A1569150 t186G03.x
C 865	8.8	30.3	37	12	A2659652	A2659652 1M0537J08	C 938	8.8	30.3	49	9	A1869979	A1869979 w163G04.x
C 866	8.8	30.3	37	12	TA35D05P	TA35D05P T. brucei	C 939	8.8	30.3	49	9	AA254773	AA254773 m23C03.x
C 867	8.8	30.3	38	10	BM046792	BM046792 BM046792	C 940	8.8	30.3	49	9	AV848976	AV848976 AV848976
C 868	8.8	30.3	38	12	A2626376	A2626376 1M0466P03	C 941	8.8	30.3	49	9	BM081077	BM081077 xc22C03.x
C 869	8.8	30.3	38	12	A2760223	A2760223 1M0553H11	C 942	8.8	30.3	49	12	BP232596	BP232596 de31h06.x
C 870	8.8	30.3	38	12	A2769444	A2769444 1M0553H11	C 943	8.8	30.3	49	12	TA322H11Q	TA322H11Q T. brucei
C 871	8.8	30.3	38	12	A2826498	A2826498 2M0102N19	C 944	8.8	30.3	50	9	AA790225	AA790225 v15d10.r
C 872	8.8	30.3	38	12	TA115F10Q	TA115F10Q T. brucei	C 945	8.8	30.3	50	9	AJ393610	AJ393610 AJ393610
C 873	8.8	30.3	39	10	R56819	R56819 HUMS000238	C 946	8.8	30.3	50	9	AU006647	AU006647 AU006647
C 874	8.8	30.3	39	10	R56819	R56819 y935h10.s1	C 947	8.8	30.3	50	9	AU0102410	AU0102410 AU0102410
C 875	8.8	30.3	39	12	A2596555	A2596555 1M0409G24	C 948	8.8	30.3	50	9	AU0102580	AU0102580 AU0102580
C 876	8.8	30.3	39	12	A2635338	A2635338 1M0491E10	C 949	8.8	30.3	50	9	AU0102655	AU0102655 AU0102655
C 877	8.8	30.3	39	12	A2814939	A2814939 2M0083C04	C 950	8.8	30.3	50	9	AU0102734	AU0102734 AU0102734
C 878	8.8	30.3	39	12	A2875800	A2875800 2M0190G04	C 951	8.8	30.3	50	9	AU0104201	AU0104201 AU0104201
C 879	8.8	30.3	40	9	AA876140	AA876140 cb39h05.s	C 952	8.8	30.3	50	9	AU0104883	AU0104883 AU0104883
C 880	8.8	30.3	40	9	AA907867	AA907867 OK79e07.s	C 953	8.8	30.3	50	9	AU0105610	AU0105610 AU0105610
C 881	8.8	30.3	40	9	AT025713	AT025713 cw11a12.s	C 954	8.8	30.3	50	9	AU0105778	AU0105778 AU0105778
C 882	8.8	30.3	40	12	TA369C08Q	TA369C08Q T. brucei	C 955	8.8	30.3	50	9	AU0107172	AU0107172 AU0107172
C 883	8.8	30.3	41	10	D19129	D19129 MUSG501345	C 956	8.8	30.3	50	9	AA341985	AA341985 hb74e05.x
C 884	8.8	30.3	41	12	A2345544	A2345544 1M0080B13	C 957	8.8	30.3	50	10	BI091761	BI091761 602858H10
C 885	8.8	30.3	41	12	A2358753	A2358753 1M0101M13	C 958	8.8	30.3	50	10	BI425400	BI425400 GI10.D06
C 886	8.8	30.3	41	12	A2368409	A2368409 1M0118A04	C 959	8.8	30.3	50	10	BI060889	BI060889 BI060889
C 887	8.8	30.3	41	12	A2467358	A2467358 1M0278M07	C 960	8.8	30.3	50	10	BE536479	BE536479 601067J24
C 888	8.8	30.3	41	12	A2579523	A2579523 1M0367G10	C 961	8.8	30.3	50	12	AZ308860	AZ308860 1M0012L13
C 889	8.8	30.3	41	12	A2772635	A2772635 1M0583L07	C 962	8.8	30.3	50	12	AZ445660	AZ445660 1M0241O07
C 890	8.8	30.3	41	12	TA174C05Q	TA174C05Q T. brucei	C 963	8.8	30.3	50	12	AA630716	AA630716 1M0484L21
C 891	8.8	30.3	42	9	AU243957	AU243957 T. brucei	C 964	8.8	30.3	50	12	A2655064	A2655064 1M0529M16
C 892	8.8	30.3	42	9	AA246094	AA246094 SWMFCAL55	C 965	8.8	30.3	50	12	A2661251	A2661251 1M0539D16
C 893	8.8	30.3	42	9	AA246094	AA246094 SWMFCAL55	C 966	8.8	30.3	50	12	A2661251	A2661251 1M0539D16

us-09-509-234c-1_1300_1328.primer.rst

Fri Jun 21 14:52:06 2002

1. 45
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U00C2M015623"
/clone_lib="Mouse 10kb plasmid U00C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GII473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

9 a 9 c 10 g

BASE COUNT
ORIGIN

Query Match 49.0%; Score 14.2; DB 12; Length 45;
Best Local Similarity 84.2%; Pred. No. 2e+04; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3;

QY 8 atgaattattacagagtttaa 26
||||| ||||| ||||| ||
Db 21 ATGAAATGTGCAGAGTGAA 3

RESULT 2
AZ801977 46 bp DNA linear GSS 16-FEB-2001
LOCUS 2M005623R Mouse 10kb plasmid U00C1M library Mus musculus genomic
DEFINITION clone U00C2M015623 R, DNA sequence.
ACCESSION AZ801977
VERSION AZ801977.1 GI:12954300
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 46)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: K column: 08
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.

AL484947 T. brucei
AZ788116 2M0035E06
AZ804243 2M0065J03
AU013584 AU013584
AZ230777 1M0056F08
AZ433664 1M0219F09
AZ388663 1M0148J15
AZ451845 1M0251I19
AZ810709 2M0076M20
AL44312 T. brucei
AL44910 T. brucei
AT744919 tti7509.x
AZ800135 2M0058C05
AZ838918 2M0134M13
AL476734 T. brucei
C02561 HUMS001246
AZ492579 1M0326H18
AZ602086 1M0420K07
AZ620113 1M0452N08
AZ938086 2M0196H02
AL495902 T. brucei
AL464014 T. brucei
AL477519 T. brucei
AA916015 og23b02.s
AZ330738 1M0056F10
AZ480878 1M0302I22
AZ814083 2M0081F12
AZ343363 1M0078K07
AZ812614 2M0079I20
AZ830000 2M0109A01
D43074 D43074 Rice
AZ366827 1M0116B17
AZ437578 1M0225I24
AZ800206 2M0058F02

1000

ALIGNMENTS

AZ853600 45 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0156E23R Mouse 10kb plasmid U00C1M library Mus musculus genomic
DEFINITION clone U00C2M015623 R, DNA sequence.
ACCESSION AZ853600
VERSION AZ853600.1 GI:13041885
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: E column: 23
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers

FEATURES

FEATURES

source

Location/Qualifiers

1. 46
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U000200060K08"
 /clone_lib="Mouse 10kb plasmid U000200060K08"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42mV; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydromedically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b) A129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

13 a 6 c 8 g 19 t

ORIGIN

Query Match 45.5%; Score 13.2; DB 12; Length 46;
 Best Local Similarity 83.3%; Pred. No. 5.5e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 atgaattacagatta 25
 ||| ||||| |||||
 Db 24 ATGCATTTTACACAGTTA 41

RESULT 3

AA154640/c

LOCUS

AA154640 49 bp mRNA linear EST 11-DEC-1996
 m44g11.r1 Bedington mouse embryonic region Mus musculus cDNA
 Clone IMAGE:540836 5' similar to SW:PAP_BOVIN P25500 POLY(A)

ACCESSION

AA154640

VERSION

AA154640.1 GI:1726278

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 49)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:327772
 Trace considered overall poor quality

FEATURES

Possible reversed clone: similarity on wrong strand
 Seq primer: -40ml3 ET
 High quality sequence stop: 1.
 Location/Qualifiers

source

1. 49
 /organism="Mus musculus"
 /strain="C57BL6 x DBA"
 /db_xref="taxon:10090"
 /clone="IMAGE:540836"
 /clone_lib="Bedington mouse embryonic region"
 /sex="pooled"
 /tissue_type="embryo"
 /dev_stage="7.5dpc"
 /lab_host="DH12S"
 /note="Organ: whole embryo; Vector: PCMV-SPORT; Site:1;
 Sall; Site:2; NotI; Cloned unidirectionally. Primer:
 Oligo dT. Gastrulating embryos were collected at 7.5dpc
 from C57BL6 x DBA matings, excluding embryos that had
 developed head folds and all extraembryonic tissues.
 Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
 Referenced in Development 121, 2479-2489 (1995)."

BASE COUNT

19 a 10 c 8 g 12 t

ORIGIN

Query Match 44.1%; Score 12.8; DB 9; Length 49;
 Best Local Similarity 87.5%; Pred. No. 8.2e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 tgaattacagatt 24
 ||| ||||| |||||
 Db 35 TGAGATTTTCAGAGTT 20

RESULT 4

BE369365

601220740F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3589857 5',

LOCUS

BE369365 45 bp mRNA linear EST 21-JUL-2000
 mRNA sequence.

ACCESSION

BE369365

VERSION

BE369365.1 GI:9314728

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 45)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

TITLE

Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs.fda.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

JOURNAL

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM8756 row: 0 column: 10

COMMENT

High quality sequence stop: 45.
 Location/Qualifiers

FEATURES

source

1. 45
 /organism="Mus musculus"
 /strain="C2EHC II (fetal)"
 /db_xref="taxon:10090"
 /clone="IMAGE:3589857"
 /clone_lib="NCI_CGAP_Lu29"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 /sex="male"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: PCMV-SPORT6; Site:1; Sall;
 Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.
 site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH

BASE COUNT 25 a 2 c 6 g 12 t

Query Match 43.4%; Score 12.6; DB 10; Length 45;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||||| | | | |
Db 7 ATGAATTTAAACATTAA 25

RESULT 5
BJ045819/c
LOCUS BJ045819 49 bp mRNA linear EST 05-DEC-2001
DEFINITION BJ045819 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL005902 3', mRNA sequence.

ACCESSION BJ045819
VERSION BJ045819.1 GI:17372516
KEYWORDS EST.
SOURCE African clawed frog.

ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 49)
AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001).
COMMENT Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source

1. .49
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL005902"
/clone_lib="NIBB Mochii normalized Xenopus neurula library"
/tissue_type="whole embryo"
/dev_stage="stage 15"

BASE COUNT 9 a 6 c 4 g 30 t

Query Match 43.4%; Score 12.6; DB 10; Length 49;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 atgaattacagagttaa 26
||||| | | | |
Db 36 AAGAACTTACATAATTAA 18

RESULT 6
A2462621/c
LOCUS A2462621 41 bp DNA linear GSS 04-OCT-2000
DEFINITION A2462621 Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0269C07 R, DNA sequence.

ACCESSION A2462621
VERSION A2462621.1 GI:10620662
KEYWORDS GSS.
SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.

Muscle whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0269 row: C column: 07

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

source

1. .41

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0269C07"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 14 a 13 c 3 g 11 t

ORIGIN

Query Match 42.1%; Score 12.2; DB 12; Length 41;

Best Local Similarity 82.4%; Pred. No. 1.5e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 atgaattacagagtt 24

||||| | | | |

Db 19 ATGAATTTATAGATT 3

RESULT 7
BJ052421
LOCUS BJ052421 48 bp mRNA linear EST 11-DEC-2001
DEFINITION BJ052421 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL041h10 3', mRNA sequence.

ACCESSION BJ052421

VERSION BJ052421.1

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

REFERENCE
 AUTHORS Kityama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara,Y.
 TITLE Expressed genes in *X. laevis* embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1. .48
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_id="NIBB Mochii normalized Xenopus neurula library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 BASE COUNT 21 a 10 c 6 g 9 t 2 others
 ORIGIN

Query Match
 Best Local Similarity 42.1%; Score 12.2; DB 10; Length 48;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 atgaattacagagta 25
 ||||| ||||| |||||
 Db 31 ATTAATGTACACAGNTA 48

RESULT 8
 BJ034980 49 bp mRNA linear EST 06-DEC-2001
 LOCUS BJ034980 NIBB Mochii normalized Xenopus neurula library Xenopus
 DEFINITION laevis cDNA clone XL031107 5', mRNA sequence.
 ACCESSION BJ034980
 VERSION BJ034980.1 GI:17396724
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM *Xenopus laevis*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 49)
 Kityama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara,Y.
 TITLE Expressed genes in *X. laevis* embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1. .49
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_id="NIBB Mochii normalized Xenopus neurula library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 BASE COUNT 17 a 9 c 9 g 13 t 1 others
 ORIGIN

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0539 row: G column: 13
 Seq primer: CACACAGCAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 34.
 Location/Qualifiers
 1. .34
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UMSCIM0559613"
 /clone_id="Mouse 10kb plasmid UMSCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 42.1%; Score 12.2; DB 10; Length 49;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 atgaattacagagt 24
 ||| ||||| |||||
 Db 40 ATGTCATTAGAGAGTT 24

RESULT 9
 A2764028 34 bp DNA linear GSS 16-FEB-2001
 LOCUS A2764028 Mouse 10kb plasmid UMSCIM library Mus musculus genomic
 DEFINITION clone UGSCIM0559613 R, DNA sequence.
 ACCESSION A2764028
 VERSION A2764028.1 GI:12878546
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM *Mus musculus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 34)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0539 row: G column: 13
 Seq primer: CACACAGCAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 34.
 Location/Qualifiers
 1. .34
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UMSCIM0559613"
 /clone_id="Mouse 10kb plasmid UMSCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 6 c 5 g 11 t

us-09-509-234c-l_1300_1328.primer.rst

Fri Jun 21 14:52:06 2002

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BASE COUNT      10 a      4 c      0 g      15 t
ORIGIN
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Best Local Similarity 77.8%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 tgaattattacagagttaa 26
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Db 26 TAAATAATTAGTGAGTTAA 9

RESULT 11
D18718 33 bp mRNA linear EST 12-DEC-1995
LOCUS MUSGS01780 Mouse 3'-directed Mus musculus domesticus cDNA clone
DEFINITION md1545 3', mRNA sequence.
ACCESSION D18718.1 GI:1100687
VERSION D18718.1
KEYWORDS EST.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kawamoto,S., Okubo,K., Yoshi,J., Katsuki,M. and Matsubara,K.
TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed
        cDNA sequencing
JOURNAL Unpublished (1995)
COMMENT Contact: Kawamoto,S., Okubo,K., Yoshi,J., Katsuki,M. and Matsubara
        ,K.
        Institute for Cellular and Molecular Biology
        Osaka University
        3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
        source
        1..33
        /organism="Mus musculus domesticus"
        /strain="C57BL/6J"
        /db_xref="taxon:10092"
        /clone="md1545"
        /clone_lib="Mouse 3'-directed"
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BASE COUNT      12 a      4 c      1 g      16 t
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Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 tgaattattacagagttaa 26
    ||||| ||| |||||
Db 31 TGAATTTTAAAGAAAAA 14

RESULT 12
TA392A110/c 36 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 392a11, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL498238
VERSION AL498238.1 GI:11873960
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE 1 (bases 1 to 36)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
        Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
        Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission

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ORIGIN

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Query Match      40.7%; Score 11.8; DB 12; Length 34;
Best Local Similarity 86.7%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 tgaattattacagagt 23
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Db 16 TGAATTTTAAAGAGT 2

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RESULT 10
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LOCUS IM0080P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0080P03 F, DNA sequence.
ACCESSION A2345539
VERSION A2345539.1 GI:10424776
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
        ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
        and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
        University of Utah Genome Center
        University of Utah
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: rdunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0080 row: P column: 03
        Seq primer: GGTGTAAACGACGCCAGT
        Class: plasmid ends
        High quality sequence stop: 29.
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        /strain="C57BL/6J"
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        /clone="UUGC1M0080P03"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of PWD42 (gi14732114|gbAF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

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FEATURES

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        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0080P03"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of PWD42 (gi14732114|gbAF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

```

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 G04t 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..36
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="392a11"

BASE COUNT
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Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 atgaattcacagagta 25
||||| ||||| |||||
Db 35 ATGACTCTCAAGTCA 18

RESULT 13
BJ014578 37 bp mRNA linear EST 05-DEC-2001
LOCUS BJ014578 MF01SSA CDNA Oryzias latipes CDNA clone MF01SSM010F09 3',
DEFINITION mRNA sequence.
ACCESSION BJ014578
VERSION BJ014578
KEYWORDS GI:17375122
SOURCE EST.
ORGANISM Japanese medaka.
Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianiichthyidae; Oryziinae; Oryzias.
1 (bases 1 to 37)
1 (bases 1 to 37)
Kohara,Y., Shin-I,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasi Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1..37
/organism="Oryzias latipes"
/strain="Hd-ir"
/db_xref="taxon:8090"
/clone="MF01SSM010F09"
/clone_lib="MF01SSA CDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"

BASE COUNT
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ORIGIN

Query Match
40.0%; Score 11.6; DB 10; Length 37;
Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 atgaattcacagagta 25
||||| ||||| |||||
Db 20 ATGACTTTGAGACTGA 37

RESULT 14
C00973 37 bp mRNA linear EST 23-JUL-1996
LOCUS C00973
DEFINITION HMG50003342 Human adult (K.Okubo) Homo sapiens CDNA, mRNA
sequence.
ACCESSION C00973
VERSION C00973.1 GI:1433203
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 37)
1 (bases 1 to 37)
Okubo,K.
BodyMap: human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
Osaka University, Suita, Osaka Pref. 565, Japan
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousakui@mbc.osaka-u.ac.jp
Human gene signature, 3'-directed CDNA sequence. We are not
submitting the same CDNA sequence redundantly to DDBJ since 1993.
for the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see
<http://www.lmbc.osaka-u.ac.jp/bodymap/>. The sequences of the clones
represented by this GS sequences is also found there.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"

BASE COUNT
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Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 atgaattcacagagta 25
||||| ||||| |||||
Db 34 ATTAATTTATTAATTTA 17

RESULT 15
D19990 37 bp mRNA linear EST 30-JUL-1996
LOCUS D19990
DEFINITION HMG500957 Human promyelocyte Homo sapiens CDNA clone mp0576 3',
mRNA sequence.
ACCESSION D19990
VERSION D19990.1 GI:500887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 37)
1 (bases 1 to 37)
Okubo,K., Fukushima,A., Yoshii,J., Miyama,T., Kojima,Y., Yoshinari
H., Arimoto,J. and Matsubara,K.
Gene expression of human promyelocytic cell line HL60 before and

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

us-09-509-234c-l_1300_1328.primer.rst

Fri Jun 21 14:52:06 2002

after induction of differentiation. A new application of 3'directed

cDNA sequencing

JOURNAL
COMMENT

Unpublished (1993)
Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Institute for Molecular and Cellular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES

Location/Qualifiers

source

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promyelocyte."

BASE COUNT
ORIGIN

15 a 4 c 2 g 16 t

Query Match 40.0%; Score 11.6; DB 10; Length 37;
Best Local Similarity 77.8%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 tgaattattacagagttaa 26
|||||
Db 31 TGAATTTTAAGAAAAA 14

Search completed: June 20, 2002, 23:06:13
Job time: 31138 sec

Fri Jun 21 08:38:18 2002

us-09-509-234c-46.rgc

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 22:09:12 ; Search time 12428.6 Seconds
(without alignments)
2160.230 Million cell updates/sec

Title: US-09-509-234C-46
Perfect score: 1283
Sequence: 1 acagctaaagaattagtgta.....tatgaattacagagattaa 1283

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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2: gb_hlg.*
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9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_ov.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
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32: em_hlg_other.*
33: em_higo_inv.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	902.2	70.3	4434	1	AF269697	AF269697 Staphyloc
4	902.2	70.3	4434	6	AX145015	AX145015 Sequence
5	900.6	70.2	1877	1	SE023713	SE023713 Staphylococ
6	876.2	68.3	1257	6	I32344	I32344 Sequence 1
7	833.4	65.0	1179	6	AX141471	AX141471 Sequence
8	811	63.2	1257	1	AF144663	AF144663 Staphyloc
9	810.6	63.2	1343	1	SHY12874	SHY12874
10	810.2	63.1	1305	6	A97484	A97484 Sequence 40
11	809.6	63.1	1343	6	A97496	A97496 Sequence 52
12	807	62.9	3446	1	SAFEA	X17688 S. aureus fa
13	797.4	62.2	303750	1	AP003133	AP003133 Staphyloc
14	797.4	62.2	346900	1	AP003362	AP003362 Staphyloc
15	797	62.1	1263	1	AF099962	AF099962 Staphyloc
16	779.4	60.7	1263	1	SHU23711	SHU23711 Staphylococ
17	774.2	60.3	1263	1	AF145332	AF145332 Staphyloc
18	774.2	60.3	1263	1	AF144661	AF144661 Staphyloc
19	749.6	58.4	1295	6	AF099965	AF099965 Staphyloc
20	741.8	57.8	1263	1	A97497	A97497 Sequence 53
21	741.2	57.8	1271	6	AF099965	AF099965 Staphyloc
22	741	57.8	1350	1	SSY12875	SSY12875 Staphylococ
23	737.8	57.5	1260	6	AF145333	AF145333 Staphyloc
24	736.6	57.4	1280	6	A97486	A97486 Sequence 42
25	731.2	57.0	1260	1	AF099963	AF099963 Staphyloc
26	717.6	55.9	1263	6	SSU66880	SSU66880 Staphyloc
27	679.6	53.0	1228	6	A97445	A97445 Sequence 1
28	670.6	52.3	1266	1	AF099967	AF099967 Staphyloc
29	670.6	52.3	1297	6	A97492	A97492 Sequence 48
30	645.4	50.3	1266	1	AF144662	AF144662 Staphyloc
31	613.8	47.8	1284	6	A97494	A97494 Sequence 50
32	607.8	47.4	1254	1	AF099966	AF099966 Staphyloc
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37	336	26.2	1284	6	A97494	A97494 Sequence 50
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39	336	25.5	341350	1	AP003137	AP003137 Staphyloc
40	326.6	25.5	54064	2	AC090968	AC090968 Staphyloc
41	309.8	24.1	2558	1	AB000222	AB000222 Staphyloc
42	297.4	23.2	4140	1	AB015195	AB015195 Staphyloc
43	297.4	23.2	347235	1	AP003361	AP003361 Staphyloc
44	295.8	23.1	2816	1	AF106851	AF106851 Staphyloc
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ALIGNMENTS

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DEFINITION	A97490				
ACCESSION	A97490				
VERSION	A97490.1	GI:6780836			
KEYWORDS					
SOURCE					
ORGANISM	Staphylococcus capitis.				
REFERENCE	Staphylococcus capitis				
AUTHORS	Bacteria; Firmicutes; Bacillus/Clostridium group;				
TITLE	Bacillus/Staphylococcus group; Staphylococcus.				
JOURNAL	1 (Phases 1 to 1283)				
FEATURES	Genetic sequences, diagnostic and/or quantification methods and				
source	DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS				
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	GALA JEAN LUC (BE); UNIV LOUVAIN (BE)				
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	/note="unnamed protein product"				

Fri Jun 21 08:38:18 2002

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TAKDVLKMSLRKNTKKVKNKREFSELSPIERFSEMDTETKEPADRDDSF
YNNRLYFKDRVLVPLAYVDYDEIIEELNNRDLNKALKDKTEKRPKNKAYNK
PDNLQQLDANQKIDKAKNLOQHEHNPISAGTFFINFEVYVYAGTSNRYRHYA
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BASE COUNT      484 a 170 c 224 g 405 t
ORIGIN
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Query Match 100.0%; Score 1283; DB 6; Length 1283;
Best local similarity 100.0%; Pred. No. 2.6e-192;
Matches 1283; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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Db 1 ACAGCTAAAGAATTAGTGACTTACTGATCAATGCCCTTATAGCCATTTACTCAGATG 60
QY 61 gaagtaattataaactaaagtgtcgaaggtacggattcacatctcctaggaattaaa 120
Db 61 GAAGTAATTATGAATTAAGTGTCTGAAGGTACGGATTACATCTCGTAGGAATTAAA 120
QY 121 aataatgacaaccaagtgatgcagatgtttataactgcgtacctgtaaatgaaatt 180
Db 121 AATAATGACACCAAGGTGATGCAGATGTTTATTAACGTCTGTACTGTAAAGAAAT 180
QY 181 tttaaatattttactcaaatccgagcagtgattgattgattgataataaaggcttgt 240
Db 181 TTTAAATATTTTACTCAATCCCGGCCAGTGTATTGATTGATTATGATAATAAGAGCTTGT 240
QY 241 cactttttttaaataagtaataatgtaaaaaagcataatgtctttacttaaga 300
Db 241 CACTTTTCTTAAATGAATTAAGTAATATGTAATAAAGCAATANTGCTTTATCTAAGA 300
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QY 421 aaaggcttcactctactcaagtaagtaagatcattcattcagtttttagatttaaaagataaa 480
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Db 541 CAAAAAATGTGTCAAGTGCCTTCTTCTATCCGAAGATGAATTACCTATCTTTAGATCA 600
QY 601 ttatggaagtactactacagaacaaaggtccgagatagatgattgtttctattat 660
Db 601 TTTATGGAGATACTACAGAAACAAAGATTCGCGATAGAGATGATAGTTTCTATAT 660
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Db 661 AATCGATATAAATACTTTAAGATAGATGATATAGTACCATTAGCATGTGTGACTTCGAT 720
QY 721 gagtatatgaagaacttaataatgaagaagatgttctttaaagaatttaataaagcg 780
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QY 781 ctcaaatatattgagaagacgtgataataagaagctttatacaaaaaagataatttt 840
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QY 901 catgtaaatgaattacactatttcagctggaattttcttcttaattccgtttgaagttgtt 960
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QY 1021 tggaaaatgataaactatgcttttagaacatggaattaaacggttaattttatggagtt 1080
Db 1021 TGGAAAATGATAAATGCTTTTAGAACATGGAATTAACCGTTATATATTTTATGGAGTT 1080
QY 1081 agtggggaactcagtggaagcgtgaagatgtaggagtaattagttcaaaaaggctat 1140
Db 1081 AGTGGGACTTCAGTGAAGCGCTGAAGATGTTAGGAGTAATTAAGTTTCAAAAAGGCTAT 1140
QY 1141 aatgctgattatgaatgattgtaggtgattttatcaagccaatacaataaactatgat 1200
Db 1141 AATGCTGATGTTATTGAATATGTTAGTGTGATTTTATCAAGCCATCAATAACTATGAT 1200
QY 1201 gcaatctataacgcacttaaaagttaaagaataagattttttaccacccaattatct 1260
Db 1201 GCAATCTATAACGCACCTTAAAGTTAAAGAATAGATTTTITACCACCAATATCT 1260
QY 1261 aattatgaatttacagagttaa 1283
Db 1261 AATTATGAATTTACAGAGTTAA 1283
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RESULT 2
AF099964 1254 bp DNA linear BCT 02-NOV-1998
LOCUS Staphylococcus capitis factor essential for methicillin resistance
DEFINITION FEMA (fema) gene, complete cds.
ACCESSION AF099964
VERSION AF099964.1 GI:3820627
KEYWORDS Staphylococcus capitis.
SOURCE Staphylococcus capitis
ORGANISM Staphylococcus capitis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Vannuffel, P., Heusterspreute, M., Bouyer, M., Philippe, M. and Gala, J.-L.
TITLE Molecular characterization of femA from Staphylococcus hominis, Staphylococcus saprophyticus and Staphylococcus haemolyticus and femA-based discrimination of staphylococcal species
JOURNAL Res. Microbiol. (1998) In press
AUTHORS Vannuffel, P., Heusterspreute, M. and Gala, J.-L.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1998) LBCM, UCL, Cios Chapelle-aux Champs 30/3046, Bruxelles 1200, Belgium
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KKAYNRKNDLQOOLDANOKIDEAKNIOGHENELPIAGVFYFNPVYVTAAGTSH
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YVGFIRPKIPMYAIYNLKKKK"
BASE COUNT      474 a      164 c      223 g      393 t
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Query Match      96.38; Score 1236; DB 1; Length 1254;
Best Local Similarity 100.0%; Freq No. 6,3e-185;
Matches 1236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 aacagtaaaagattagacttactgaacaaagccttaagcatttactacagatg 60
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OY 61 gaaggtaattatgaactaaagttgcgaaggttagcgattcacatcgttagaattaa 120
Db 79 GAAGGTAAATATGAACTTAAAGTGTCTGAAGTACGATTCACACATCTGTAGAAATTA 138
OY 121 aataatgcaacaaagtgatgagacatgattataacgtcgtacccgtataaatt 180
Db 139 AATAATGACAAACGAGTGCAGATGTTATTATTAATCTGCTACCTGTAATGAAAT 198
OY 181 tttaaatatttactcaaaatcgggggcgaagtgattgataataaagagctgtt 240
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OY 241 caattttctttaaagtaagtaaaatgtaaaagcataatgcttattactaaga 300
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OY 301 gttagccctattcttcttcaactaacttaactgacggtagaattatggaatgct 360
Db 319 GTTAGCCCTATCTCTTATCAATACTTAAATCATGACGCGGAATTAATGGAATGCT 378
OY 361 ggccatgattgttttcaataagatgaaagattagattggaacatgaagcttcat 420
Db 379 GGCCATGATGTTGTTTCAATTAAGTAAGTAAGTATGAAATGAAAGCTTTCAT 438
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OY 481 acggctaaagatgactcaaaagaaatgatatgattaaagaagcgaataactaagaagta 540
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Db 559 CAAAAAATAGTGTCAAAGTCCGTTCCATATCCGAAGATGATTAATACCTTTAGATCA 618
OY 601 ttaatggaagatactcaagaagaagatcgccgagtagagatgatagtttctatcat 660
Db 619 TTATGGAAGATACTACAGAAACGAAAGATTCCGCCGATAGATGATGTTCTTATAT 678
OY 661 aatgattaaatactttaaagatagattagatcacattagatattttagctcgat 720
Db 679 AATGATTAATAATACCTTAAAGATAGAGTATTAGTACCTTATGCAATTTGTAGCTCGAT 738
OY 721 gagatataagaaacttaataagaaagatgattcttaataaagatttaataagcgc 780
Db 739 GAGTATATGAAAGACTTATATATGAAGAGATGTTCTTAATAAAGATTTAAATAGGCG 798

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OY 781 ctcaagatattggaagagagaccgtataataagaagcttatacaaaagagataatcct 840
Db 799 CTCAAAGATATTGAGAGAGACCTGATTAAGAAACCTTATACAAAGAGATAACTT 858
OY 841 caacaacaattagatgcaaatcaacaanaaattatgaagctaaanaacttaacaaga 900
Db 859 CAACAACAATTGATGATGCAAAATCAACAAAATATGATGAGCTTAAACCTTACACAGAA 918
OY 901 catgtaagaattaccattcattcagctgataattcttcaataaccgtttgaagttgt 960
Db 919 CATGTAATGATTAATCAATTTAGCGGATATTCTTCATTAATCCGTTTAATCTTCT 978
OY 961 tattaacaggttggaacatcgaaatcgattatgtaactatgcgcgaagttagaaatca 1020
Db 979 TATTACGAGGTGGCCACATCAATGATGTTATGCTGATCGCGGAAGATATGCAATTTCA 1038
OY 1021 tggaaatgataactatgactttagaacaatgaaatnaacgattataatttttagagatt 1080
Db 1039 TCGAAATGATTAATCAATCTTTAGAACATGAAATTAACCGTTATATTTTATGAGATT 1098
OY 1081 agtgggagcttcagtgaaagcgtgaagatgtagagtaattaagttcaaaaagctat 1140
Db 1099 AATGGGAGCTTCAGTGAAGACCTGATGATGTAGAGTATGAGTAAATTAATCAAAAAGCTAT 1158
OY 1141 aatgctgatttattgaatgattgatttataaagcaatacaataaactatgatt 1200
Db 1159 AATGCTGATGTTATGAAATATGATGATTTTATCAAGCAATCAATCAATCAATGAT 1218
OY 1201 gcaatctataacgacttaaaagttaaagaatag 1236
Db 1219 GCAATCTATTAAGCACTTAAAGTTAAAGTAATAG 1254

RESULT 3
AF269697 4434 bp DNA linear BCT 01-ANG-2000
LOCUS Staphylococcus epidermidis strain SN1 clone step.1017f06 genomic
DEFINITION sequence.
ACCESSION AF269697
VERSION AF269697.1 GI:9623592
KEYWORDS Staphylococcus epidermidis.
SOURCE Staphylococcus epidermidis.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 4434)
AUTHORS Kimmerly W.J., Taylor J., David., Nelsen A.J., Godlevski M.M.,
Rubino M.A., Nelson F.J., Rivers P.R., Toriella Miller I.,
Listendee S., Ashanti C., Altschuller G., Mammo L., Shepherd N.S.,
Fuchs R., Fleming T., Guan X., Du L., Cain D.H., Miller G.S. and
Furdon P.J.
TITLE Transposon-mediated sequencing of the Staphylococcus epidermidis
genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4434)
AUTHORS Taylor J., David., Kimmerly W.J., Nelsen A.J., Godlevski M.M.,
Rubino M.A., Nelson F.J., Rivers P.R., Toriella Miller I.,
Listendee S., Ashanti C., Altschuller G., Mammo L., Shepherd N.S.,
Fuchs R., Fleming T., Guan X., Du L., Cain D.H., Miller G.S. and
Furdon P.J.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
Drive, Research Triangle Park, North Carolina 27709-3390, USA
FEATURES
source location/Qualifiers
1. 4434
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/strain="SN1"
/db_xref="taxon:1282"
/clone="step.1017f06"
BASE COUNT 1676 a 554 c 819 g 1385 t
ORIGIN

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Query Match 70.3%; Score 902.2; DB 1; Length 4434;
 Best Local Similarity 82.0%; Pred. No. 1.2e-132;
 Matches 1052; Conservative 0; Mismatches 228; Indels 3; Gaps 1;

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 DB 2885 ACAGCTAAAGAATTAGTGACTTTACTGATCGTATGACATATAGTCATTTTACACAATG 2944

QY 61 gaaggttaattgaacttaagtgtcgaaggtgaaggttaacatctcgtaggaattaa 120
 DB 2945 GAAGGTAAATGAAGTAAAGGTGCTGAAGGTACCGAGTACACATTTAGTGAATTA 3004

QY 121 aataatgacacaaagtgatgacagatgtttattaaactgtgtacgtgtaagaaat 180
 DB 3005 AATAATGAACGAAGTGAATGACAGTGTGTTTAAACAGCTGTCTGTGAATGA 3064

QY 181 tttaaatattttactcaaatcgcggccagtgattgattgataataaagagctgtt 240
 DB 3065 TTTAAATATTTTATTCATTCGCGTCCAGTAAAGTAAATGAATGAAGAGCTGTGA 3124

QY 241 caotttttcttaagtaattgaataatgtataaagacataattgcttttactcaaga 300
 DB 3125 CATTTTCTTAAAGTAATGAGTAATATGTAATAATATATATTTTATATTTA 3184

QY 301 gttgacctattcttccattatcaacttaactaaatcatgacgtgtaagaaatgct 360
 DB 3185 GTTGACCCATACCTTCCATATCAATTTTAAATCATGAGGAGAAATAACTGGAATGCA 3244

QY 361 ggcacatgattgttttcaataagatggaagattgaggttgaacatgaagctttcat 420
 DB 3245 GGTCAATGATGATTTTGTGATTAAGTATGAGAGTTAGAGATTAACACGAAGGATTCAC 3304

QY 421 aaaggttccattcttcaagtaagtaagatacatcattcagttttagatttaaaagataa 480
 DB 3305 AAAGGATTGATCTGTATTAACAACTGATATCTGTTCTTAATTTAGCAACAAA 3364

QY 481 acggttaagatgtactcaaggaatggatgtttaaagaagcgtataactaagaagta 540
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QY 541 caaaatggtgtcgaagtccttccattccatccgaagatgaattacattctttagatca 600
 DB 3425 AGAAAAATGGAGTAAAGTCCGCTTTTATCTGAAGAAGGTTACCTATATTTAGTCA 3484

QY 601 tttaggaagatactacagaaagcgaaggttcgcgcatagatgatttctattat 660
 DB 3485 TTTATGGAGGATACCTCTGAACATAAGATTTTGCAGATAGAGATAGTTTATTTAC 3544

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 DB 3545 AACAGATTCAACATTTAAGACCGTGTTTTAGTACCACATGCTTATTTTATTTTAT 3604

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 DB 3605 GAGTATATAGAGAACTAAATATGAAGAATGTGCTTATTAAGATATATTAAGACT 3664

QY 781 ctcaagatattgagaagagacattgataaagaagcgttatacaaaaagagataactt 840
 DB 3665 TTAAAGACATTGGAACCTCCGAGATTAAGAGCAATACACAAAGGAAATTTA 3724

QY 841 caacaacatttagatgcaaatcaacaaaattgataagcgttaaaacttacaacagaa 900
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QY 901 catggttaattgaactatttcaactgtgatttcttatttaactcgtttgaagttgtt 960
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QY 1261 aattatgaattttacagaggttaa 1283
 DB 4142 AATTATGAATTTACAGAGTTAA 4164

RESULT 4
 AX145015
 LOCUS AX145015 4434 bp DNA linear PAT 31-MAY-2001
 DEFINITION Sequence 3737 from Patent WO0134809.
 ACCESSION AX145015
 VERSION AX145015.1 GI:14283580
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial construct.
 REFERENCE 1 (bases 1 to 4434)
 AUTHORS Kimmerly, W.J.
 TITLE Staphylococcus epidermidis nucleic acids and proteins
 JOURNAL Patent: WO 0134809-A 3737 17-MAY-2001;
 GLAXO GROUP LIMITED (GB)
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 Location/Qualifiers
 source
 1. 4434
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="synthetic nucleic acid sequence"

BASE COUNT 1676 a 554 c 819 g 1385 t
 ORIGIN

Query Match 70.3%; Score 902.2; DB 6; Length 4434;
 Best Local Similarity 82.0%; Pred. No. 1.2e-132;
 Matches 1052; Conservative 0; Mismatches 228; Indels 3; Gaps 1;

QY 1 acagctaaagaatttagtgactttactgacaaatgcctttagccattttactcagatg 60
 DB 2885 ACAGCTAAAGAATTAGTGACTTTACTGATCGTATGACATATAGTCATTTTACACAATG 2944

QY 61 gaaggttaattgaacttaagtgtcgaaggtgaaggttaacatctcgtaggaattaa 120
 DB 2945 GAAGGTAAATGAAGTAAAGGTGCTGAAGGTACCGAGTACACATTTAGTGAATTA 3004

QY 121 aataatgacacaaagtgatgacagatgtttattaaactgtgtacgtgtaagaaat 180
 DB 3005 AATAATGAACGAAGTGAATGACAGTGTGTTTAAACAGCTGTCTGTGAATGA 3064

QY 181 tttaaatattttactcaaatcgcggccagtgattgattgataataaagagctgtt 240
 DB 3065 TTTAAATATTTTATTCATTCGCGTCCAGTAAAGTAAATGAATGAAGAGCTGTGA 3124

QY 241 caotttttcttaagtaattgaataatgtataaagacataattgcttttactcaaga 300
 DB 3125 CATTTTCTTAAAGTAATGAGTAATATGTAATAATATATATTTTATATTTA 3184

QY 301 gttgacctattcttccattatcaacttaactaaatcatgacgtgtaagaaatgct 360
 DB 3185 GTTGACCCATACCTTCCATATCAATTTTAAATCATGAGGAGAAATAACTGGAATGCA 3244

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OY 361 ggcacatgattggttttcaataagatggaagaattagatttgacaatgaagccttcac 420
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Db 3245 GGTCAGATGGATTTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 3304

OY 421 aaaggtctccatccatccatccatccatccatccatccatccatccatccatccat 480
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Db 3305 AAAGATTTGATCTCTGTTTAAACCCGATCATCTGTTCTTAATTTAGCAAAACAA 3364

OY 481 acggtctaaagatgactcaagaagatgactgactgactgactgactgactgactgact 540
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OY 541 caaaaaaatggtgcaagtcgttccatccgaagaatgactgactgactgactgactgact 600
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OY 601 tttaatggaatactcaagaagaagaagtcgcgcgactgactgactgactgactgact 660
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Db 3665 TTTAAAGACATTTGAGAAACCTCCAGAGATTAAGAAACGACATTAACAAAGAAATTT 3724

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Db 3725 GAACAAACATCGATGCAATGCAAGAAATTAATGAGATTAAGATTAAGATTAAGATTA 3784

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OY 1021 tgaataatgataactgactgactgactgactgactgactgactgactgactgactgact 1080
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Db 4085 AACATTTATGAAACCTTAATAAACTTAAGAAATGAGAAATGAGAAATGAGAAATGAG 4141

OY 1261 aattatgaatttagaagttaa 1283
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Db 4142 AATTATGAAATTTACAGAGTTAA 4164

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RESULT 5
SERU23713
LOCUS SERU23713 1877 bp DNA linear BCT 04-FEB-1997
DEFINITION Staphylococcus epidermidis factor essential for methicillin
resistance FEMA (fema) gene, complete cds.
ACCESSION U23713
VERSION U23713.1 GI:1815617
KEYWORDS

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SOURCE Staphylococcus epidermidis.
ORGANISM Staphylococcus epidermidis;
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; staphylococcus.
REFERENCE 1 (bases 1 to 1877)
AUTHORS Alborn, W.E., Jr., Hoskins, J., Una, S., Plokovitsch, J.E., Hayes, C.A.,
Dotz, J.E., Yeh, W.K., and Skatrud, P.L.
TITLE Cloning and characterization of femA and femB from Staphylococcus
epidermidis
JOURNAL Gene 180 (1-2), 177-181 (1996)
MEDLINE 97128824
REFERENCE 2 (bases 1 to 1877)
AUTHORS Alborn, W.E., Jr.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-1995) William E. Alborn, Jr., Lilly Corporate
Center, Eli Lilly and Company, Indianapolis, IN 46285-0428, USA
FEATURES
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/clone="pSJ180"
367..1635
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367..1635
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/feature="factor essential for methicillin resistance"
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 DEFINITION Sequence 1 from patent US 5587307.
 ACCESSION I32344
 VERSION I32344.1 GI:1823135
 KEYWORDS Unknown.
 SOURCE

ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1257)
 AUTHORS Alborn,W.E. Jr., Hoskins,J., Skatrud,P.L. and Unal,S.
 TITLE fema gene of staphylococcus epidermidis, fema protein, and vectors
 and microorganisms comprising the fema gene
 JOURNAL Patent: US 5587307-A 1 24-DEC-1996;
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 Best Local Similarity 81.9%; Pred. No. 1.8e-128;
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RESULT 8

AF144663

LOCUS AF144663

DEFINITION *Staphylococcus warneri* factor essential for methicillin resistance (fema) gene, complete cds.

ACCESSION AF144663

VERSION AF144663.1

1257 bp

DNA

linear

BCT 01-JUN-1999

GI:4929302

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KEYWORDS
SOURCE
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    Staphylococcus warneri.
    Bacteria; Firmicutes; Bacillus/Clostridium group;
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REFERENCE
  1 (bases 1 to 1257)
  Vannuffel,P., Heusterspreute,M. and Gala,J.-L.
  Cloning and characterization of femA genes from Staphylococci
  species
  JOURNAL
    Unpublished
REFERENCE
  2 (bases 1 to 1257)
  Vannuffel,P., Heusterspreute,M. and Gala,J.-L.
  Direct Submission
  TITLE
    Submitted (21-APR-1999) LBCM, UCL 3046, Cios Chapelle-aux-Champs,
  JOURNAL
    30, Bruxelles 1200, Belgium
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Fri Jun 21 08:38:18 2002

us-09-509-234c-46.rge

Page 9

AUTHORS Vannuffel, P.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1343)
AUTHORS Vannuffel, P.
TITLE Direct Submission
JOURNAL Submitted (30-APR-1997) P. Vannuffel, University of Louvain Medical School, Laboratoire de Genetique Moleculaire, UCL-GENO-5225, Avenue E. Mounier 52, Brussels 1200, BELGIUM

FEATURES
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LOCUS Sequence 40 from Patent W0916780.
DEFINITION A97484
ACCESSION A97484.1 GI:6780830
VERSION
KEYWORDS
SOURCE
ORGANISM
Staphylococcus haemolyticus.
Staphylococcus haemolyticus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
1 (bases 1 to 1305)
Gala, J. and Vannuffel, P.
GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
Patent: WO 9916780-A 40 08-APR-1999;
JOURNAL
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES
source Location/Qualifiers
1. 1305
/organism="Staphylococcus haemolyticus"

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VERSION	A97496.1	GI:6780842	
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ORGANISM	Staphylococcus hominis		
REFERENCE	Bacteria; Firmicutes; Bacillus/Clostridium group;		
AUTHORS	Bacillus/Staphylococcus group; Staphylococcus.		
TITLE	1 (bases 1 to 1343)		
	Gala, J. and Vannuffel, P.		
	GENERIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND		
JOURNAL	DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS		
	Patent: WO 9916780-A 52 08-APR-1999;		
	GALA JEAN LUC (BE); UNIV LOUVAIN (BE)		
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Fri Jun 21 08:38:18 2002

us-09-509-234c-46.19e

Page 11

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ORIGIN

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Best Local Similarity 78.6%; Pred. No. 5e-118;
Matches 968; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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LOCUS S. aureus factor essential for expression of methicillin resistance
DEFINITION (fema) gene, complete cds, and trpA gene, 3' end.
ACCESSION X17688 M23918
VERSION X17688.1 GI:46579
KEYWORDS femA protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 3446)
Bacillus/Staphylococcus group; Staphylococcus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
AUTHORS Berger-Baechli, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3446)
Berger-Baechli, B., Barberis-Maino, L., Straessle, A. and Kayser, F. H.
Fema, a host-mediated factor essential for methicillin resistance
in Staphylococcus aureus: molecular cloning and characterization
Mol. Gen. Genet. 219 (1-2), 263-269 (1989)
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by B. Berger-Baechli, 11-Apr-1989.
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TITLE Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*

JOURNAL Lancet 357 (9264), 1225-1240 (2001)

MEDLINE 21311952

REFERENCE 2 (bases 1 to 303750)

AUTHORS Aoki, K., Oguchi, A., Hosoyama, A., Nagai, Y., Kuroda, M., Hiramatsu, K.

TITLE Direct Submission
JOURNAL Submitted (30-JAN-2001) Kenichi Aoki, National Institute of
Technology and Evaluation, Biotechnology Center; 2Chome 49-10
Nishihara, Shibuya-ku, Tokyo 151-0066 Japan
(E-mail: aoki-kenichi2@meti.go.jp, URL: http://www.bio.nite.go.jp/
Tel: 81-3-3481-1972, Fax: 81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701012.

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Qy	1201	caactataacgacttaaaaaagttataaagaataatagattttttaccacacacattatct	1260
Db	184422	GCAGCATATACCCGCTTAAAAAGCTTAA-AGACAGAAATTTTTAGGAAGGAATTTATCA	184480
Qy	1261	aattatgaattttacagagtttaa	1283
Db	184481	AAACATGAATTTACAGAGTTAA	184503
RESULT 14			
AP003362			
Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete			
sequence, section 5/9.			
AP003362 BA000017			
AP003362.2 GI:14247083			
Staphylococcus aureus subsp. aureus Mu50 (sub-species:aureus Mu50, strain:Mu50) DNA.			
Staphylococcus aureus subsp. aureus Mu50			
Bacteria: Firmicutes; Bacillus/Clostridium group;			
Bacillus/Staphylococcus group; Staphylococcus.			
1 (sites)			
Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,			
Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M.,			
Matsunaru, H., Maruyama, A., Murakami, H., Hosoyama, A.,			
Mizutani, G. Y., Takahashi, N. K., Sawano, T., Inoue, R., Kaito, C.,			
Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J.,			
Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C.,			
Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K.			
Whole genome sequencing of methicillin-resistant Staphylococcus			
aureus			
TITLE			

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	/db_xref="GI:13701022"		
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	/gene="cfzE"		
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	/gene="cfzE"		
	/note="ORFID:SA1065		
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IKMERQLNFDIENDGVNTDARVCVENGATMLVTGSFFFKQEDYKKYVQALKG"			
Query Match 52.2%; Score 797.4; DB 1; Length 303750;			
Best Local Similarity 76.9%; Pred. No. 1.3e-116;			
Matches 986; Conservative 0; Mismatches 296; Indels 1; Gaps 1;			
Qy	1	acagctaaagatttagtacttactatcaaatgcttacttagccatttactcagatg	60
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Qy	361	ggccatgattggttttccaataagatggagaatttaggatttgaacatgaaggtcttcat	420
Db	183582	GGTAATGATTGTTCTTTGATAAATGAGTAACCTTAGGATTGAACATATGCTGATCCAT	183641
Qy	421	aaagcttccatccctatcttaccagaagatattcattcattgattttagatttaaaagataaa	480
Db	183642	AAAGGATTTGATCTCTGCTGCTACAAATTCGTTATCACTCAGTGTGTAGATTTTAAAGATAA	183701
Qy	481	acgctaaagattgactcaaaaggaatgagtagtttaagaagaagcgtataactaagaagta	540
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 DB 67071 TTTATGGAAGATPACGTCAGAAATCAAAAGCTTTTGCTGATCGTATGACAAATTTTACTAC 67130
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 QY 721 gagtattatgaacacttaataatgaagagatgttcttaataaagatttaaaataagcg 780
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 DB 67311 CAACAACAATCTGATGCTAATGAGCAAAAGATTGAAGAAGTTAAACCTTACAGAAGAA 67370
 QY 901 catgtaatgaattcaactatttcagctggatatttcttcaatttcogtttgaattgtt 960
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 QY 1141 aatcgatgattttgaatatgttagtgattttatcaagccaatcaaaaacctatgtat 1200
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 QY 1201 gcaatctataacgcacttaaaaagtttaagaagaatagatttttttcaaccaccattatct 1260
 DB 67671 GCACGATATACCGCACTTAAAAAGTTAA-AGACAGAAATTTTTTAGGAGGGAATTATCA 67729
 QY 1261 aattatgaattttcacagagttaa 1283
 DB 67730 ABACTGAATTTTACAGAGTTAA 67752

us-09-509-234c-46.rge

Fri Jun 21 08:38:18 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:46:04 ; Search time 1139.49 Seconds
(without alignments)
1933.147 Million cell updates/sec

Title: US-09-509-234C-46
Perfect score: 1283
Sequence: 1 acagctaaagaattagttga.....tatgaattacagagttaa 1283

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	1283	100.0	20	Staphylococcus cap
2	902.2	70.3	22	S. epidermidis gen
3	876.2	68.3	1257	Staphylococcus epi
4	833.4	65.0	1179	S. epidermidis ope
5	810.2	63.1	1305	Staphylococcus hae
6	800.8	62.4	20	Staphylococcus hom
7	749.6	58.4	20	Staphylococcus xyl
8	741.2	57.8	20	Staphylococcus sep
9	736.6	57.4	20	Staphylococcus lug

10	679.6	53.0	1328	20	AAK37797	Staphylococcus sp.
11	670.6	52.3	1297	20	AAK37802	Staphylococcus sch
12	613.8	47.8	1284	20	AAK37803	Staphylococcus sci
13	507	39.5	3115	22	AAH53994	S. epidermidis gen
14	343.8	26.8	6528	21	AAZ49723	Staphylococcus sim
15	326	25.4	3271	18	AAV74747	Staphylococcus aur
16	317.6	24.8	3821	18	AAV74615	Staphylococcus aur
17	297.4	23.2	1470	20	AAZ22843	Staphylococcus aur
18	289.4	23.2	1470	20	AAZ15882	Staphylococcus aur
19	289.4	22.6	1245	23	AAZ55125	Staphylococcus epi
20	283.4	22.1	1251	15	AAQ74775	S. epidermidis ope
21	283.4	22.1	1254	22	AAH52401	Essential Staphylo
22	277.2	21.6	453	22	AAZ08009	Staphylococcus aur
23	277.2	21.6	453	22	AAZ08009	Staphylococcus aur
24	277.2	21.6	453	22	AAZ08009	S. epidermidis gen
25	271	21.1	2453	22	AAH55015	Essential Staphylo
26	256	20.0	410	21	AAZ26855	Staphylococcus aur
27	256	20.0	410	22	AAZ08006	Staphylococcus aur
28	256	20.0	410	22	AAZ08006	Staphylococcus aur
29	251.6	19.6	1257	23	AAZ51636	Staphylococcus aur
30	251.6	19.6	1260	23	AAZ54419	Staphylococcus aur
31	250	19.5	1260	20	AAZ07088	Staphylococcus aur
32	250	18.5	1260	20	AAZ07091	Staphylococcus aur
33	225.8	17.6	514	18	AAZ80799	Staphylococcus aur
34	221.2	17.2	400	21	AAZ26853	Essential Staphylo
35	221.2	17.2	400	22	AAZ08004	Staphylococcus aur
36	221.2	17.2	400	22	AAZ08004	Staphylococcus aur
37	211.4	16.5	420	20	AAZ89751	Synthetic DNA frag
38	166.8	13.0	1281	23	AAZ52835	Enterococcus faeca
39	156.8	12.4	1221	18	AAZ74940	Staphylococcus aur
40	156.8	12.2	543	22	AAZ71123	C. glutamicum SRP
41	155.8	12.1	10194	20	AAZ13028	Enterococcus faeca
42	144	11.2	795	23	AAZ50908	Staphylococcus zif
43	113	8.8	1230	20	AAZ76141	Staphylococcus zif
44	113	8.8	6804	20	AAZ76160	6.8kb EcoRI fragme
45	111.2	8.7	158	18	AAZ76848	Staphylococcus aur

ALIGNMENTS

RESULT 1
ID: AAK37801 standard. DNA: 1283 BP.

AAK37801:

09-JUL-1999 (first entry)

Staphylococcus capitis FemA DNA.

FemA: identification; detection; therapy; infection; femB; amplification; genotyping; gram positive bacterial; vaccine; ss.

Staphylococcus capitis.

Key: Location/Qualifiers
CDS 1..1283 /tag- a
FT /product= "FemA"
FT /note= "partial sequence, no start or stop codon"

XX WO9916780-A2.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98NC-BE00141.
XX PR 26-SEP-1997; 97EP-0870146.
XX PA (BEA-) BELGIAN MIN NAT DEFENCE.
XX PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.

Fri Jun 21 08:38:19 2002

Db 601 ttatggaagatactacagaaacgaagaggttcgcatagagatgtagtatttcttattat 660
 Qy 661 aatcgattataaacttttaagatagatagatttagtaccattagcatatgttgacttcgat 720
 Db 661 aatcgattataaacttttaagatagatagatttagtaccattagcatatgttgacttcgat 720
 Qy 721 gagtatatgaagaacttaataatgaagaagatgttcttaataaagattttaaataaggcg 780
 Db 721 gagtatatgaagaacttaataatgaagaagatgttcttaataaagattttaaataaggcg 780
 Qy 781 ctcaagatattgaagaagcctgataataaagaagcttatacaaaaagagataatctt 840
 Db 781 ctcaagatattgaagaagcctgataataaagaagcttatacaaaaagagataatctt 840
 Qy 841 caacaacattagatgcataacacaaaattgatgaagctaaataaacttacaagaagaa 900
 Db 841 caacaacattagatgcataacacaaaattgatgaagctaaataaacttacaagaagaa 900
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 Db 1021 tggaaaatgataaactatctttagaacaatggaattaaacccgttataatttttggagtt 1080
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 Db 1081 agtgggacttcagtgaaagcgtgaaagatgtaggagtaatttaagttcaaaaaggctat 1140
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 Db 1141 aatgctgattgtattgaatgtaggtgattttatcaagccaatcaataaactatgat 1200
 Qy 1201 gaaactataacgcacttaaaaagtttaagaataagatttttttaccacccaattatct 1260
 Db 1201 gaaactataacgcacttaaaaagtttaagaataagatttttttaccacccaattatct 1260
 Qy 1261 aattatgaaatttaccagagttaa 1283
 Db 1261 aattatgaaatttaccagagttaa 1283

RESULT 2
 AAH54373
 ID AAH54373 standard; DNA: 4434 BP.
 AC AAH54373;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3737.
 XX
 KW Staphylococcus epidermidis S81 strain; infection; diagnosis;
 XX vaccination; endocarditis; ds.
 OS Staphylococcus epidermidis.
 XX
 PN WO200134809-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 09-NOV-2000; 2000WO-US30782.
 XX
 PR 09-NOV-1999; 99US-0164258.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Kimmerly WJ;

PI Gala J, Vannuffel P;
 XX WPI; 1999-287521/24.
 DR P-PSDB; AAY08218.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 XX Claim 21; Fig 9a-b; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 1283 BP; 484 A; 170 C; 224 G; 405 T; 0 other;
 Query Match 100.0%; Score 1283; DB 20; Length 1283;
 Best Local Similarity 100.0%; Pred. No. 3.7e-242;
 Matches 1283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 acagctaaagatttagtacttactgatacaaatgcttattagccattttactcagatg 60
 Db 1 acagctaaagatttagtacttactgatacaaatgcttattagccattttactcagatg 60
 Qy 61 gaaggttaattgaactaaagtgtcgaagtcagcagatcaacatctcaggaataaa 120
 Db 61 gaaggttaattgaactaaagtgtcgaagtcagcagatcaacatctcaggaataaa 120
 Qy 121 aataatgacacaaagtgatgcagatgttttataactcgtcaccgttaagtgaatt 180
 Db 121 aataatgacacaaagtgatgcagatgttttataactcgtcaccgttaagtgaatt 180
 Qy 181 tttaaatatttttactcaaatcgggcccagtgattgattatgataataaagagcttctt 240
 Db 181 tttaaatatttttactcaaatcgggcccagtgattgattatgataataaagagcttctt 240
 Qy 241 cacttttttttataatgaattaaatgataatgtataaagaacataattgtctttatcaaga 300
 Db 241 cacttttttttataatgaattaaatgataatgtataaagaacataattgtctttatcaaga 300
 Qy 301 gttgacccattatctccttatacaattcaatcattgacggtgaaattattggaattgct 360
 Db 301 gttgacccattatctccttatacaattcaatcattgacggtgaaattattggaattgct 360
 Qy 361 ggcctagtggtttttcaataagatggaagattgattgaaacatgaaggtctttcat 420
 Db 361 ggcctagtggtttttcaataagatggaagattgattgaaacatgaaggtctttcat 420
 Qy 421 aaaggttccatctatttacaagtaagatcatctcagtttttagatttaaaagataaa 480
 Db 421 aaaggttccatctatttacaagtaagatcatctcagtttttagatttaaaagataaa 480
 Qy 481 acgggttaagatgattactcaaggaattgatttttaagaagcgttaacttaagaagata 540
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 Db 541 caaaaaatggttcaagtcggttctcctatccgaagatgaattaccattcttttagatca 600
 Qy 601 ttatggaagatactacagaaacgaaggttcgcccagatagatgattttctattat 660

DR	XX	WPI; 2001-316495/33.
NR	XX	Nucleic acids encoding polypeptides from <i>Staphylococcus epidermidis</i> ,
PT	XX	useful for vaccinating against infections, e.g. endocarditis -
PS	XX	Claim 8: Page 1358-1360; 2188bp; English.
CC	XX	AH52304 to AH53970 represent nucleic acids (I) encoding polypeptides
CC	XX	(II), given in AAG61454 to AB83120, from <i>Staphylococcus epidermidis</i> .
CC	XX	(I) and (II) can have antibacterial activity and therefore can be used
CC	XX	in vaccination. The nucleic acids (I) may be used to produce the
CC	XX	S. epidermidis polypeptides (II) via the production of vectors
CC	XX	containing them which are used to produce hosts cells which express the
CC	XX	polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC	XX	used to vaccinate subjects and to raise antibodies against the bacteria.
CC	XX	The polypeptides may also be used to assay for other inhibitors of their
CC	XX	activity and therefore identify compounds that may be used for the
CC	XX	treatment of S. epidermidis infections, e.g. endocarditis. AH53971 to
CC	XX	AH55096 represent specifically claimed S. epidermidis genomic DNA
CC	XX	polynucleotide sequences from the present invention. AH55091 to
CC	XX	AH55096 represent oligonucleotide sequences and primers which are used
CC	XX	in the exemplification of the present invention.
CC	XX	N.B. The present invention specifically claims all the polynucleotide
CC	XX	sequences given in the sequence listing of the present specification,
CC	XX	however the sequence listing only goes up to SEQ ID NO:4454 so even
CC	XX	though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
CC	XX	no sequences are present for SEQ ID NO:4455 to 4464.
SO	XX	Sequence 4434 BP; 1676 A; 554 C; 819 G; 1385 T; 0 other;
Query Match	70.3%; Score 902.2; DB 22; Length 4434;	
Best Local Similarity	82.0%; Pred. No. 1-Se-167;	
Matches 1052; Conservative	0; Mismatches 228; Indels	3; Gaps
QY	1	acagcaagaatttagtgacttactgtatcgaatgcgcttaagccatttactcatagt 60
DB	2885	acaagctaagaatttagtgacttactgtatcgaatgcgcttaagccatttactcatagt 2944
QY	61	gaagcaattactgaactaaagttcgctgaaggtaagatacacatcgtlagaataaa 120
DB	2945	gaagcaattactgaactaaagttcgctgaaggtaagatacacatcgtlagaataaa 3004
QY	121	aataatgaaccnaagtgattgcagcatgtttattacctgtcgtacctgtatgaaatt 180
DB	3005	aataatgaaccnaagtgattgcagcatgtttattacctgtcgtacctgtatgaaatt 3064
QY	101	tttaaatattttactcaaacgcggcgccagtgattgttatgtgataaagaagcttgt 240
DB	3065	tttaaatattttactcaaacgcggcgccagtgattgttatgtgataaagaagcttgt 3124
QY	241	cactcttcctttaatgaattaagtaaatatgtataaaaaagcataatgttcttatcaga 300
DB	3125	catttttctttaatgaattaagtaaatatgtataaaaaagcataatgttcttatcaga 3184
QY	301	gtgacctatcttcttataccaacttaataatcatgatgcgtgaaattatttgaattgt 360
DB	3185	gtgacctatcttcttataccaacttaataatcatgatgcgtgaaattatttgaattgt 3244
QY	361	ggcagatattggtttttaaataaagtaggaatttgagttgagttgaagaagctttcat 420
DB	3245	ggcagatattggtttttaaataaagtaggaatttgagttgagttgaagaagctttcat 4304
QY	421	aaagcttcacccctactttaagaatgaatcatctcgttttgaattttaaagaataa 480
DB	3305	aaagcttcacccctactttaagaatgaatcatctcgttttgaattttaaagaataa 3364
QY	481	acggctaagaattactcaaaaggaatgatatgtttaagaagcgtataactaagaagta 540
DB	3365	agtgtaattgcttttaaaaaacatgtagtitttgaagaagcgtataactaagaagtt 3424
QY	541	caaaaataatggttcaaaagtcggtttcttactacgaagatgaattactatctttagatca 600

Accession	Gene	Position	Sequence	Length
Db 3425	aaganaaaygagttcaaaagtcgcttttaaccgaaagagttactctatatttgatca	3484		11
Qy 601	tttatggaagatctacacgaagaagagttccgcatagatgagatgtattctaat	660		11
Db 3485	tttatggaagatctacacgaagaagagttccgcatagatgagatgtattctaat	3544		11
Qy 661	aatcgattaaavactttaagatagatgtatgaccattgacatgtgtgcttgat	720		11
Db 3545	aacgattcaaacattataaagacgctgttttagtaccattgacctatatttaatt	3604		11
Qy 721	gagtatatcgaaagacttaataatgaaagagatgttttaataagatttaaaagag	780		11
Db 3605	gagtatatcgaaagacttaataatgaaagagatgttttaataagatttaaaagag	3664		11
Qy 781	cccaagaattttgagagagagcctcgtaataagaagcttatcaacaagaagatacct	840		11
Db 3665	ttaaaagacatttgaagaagcttcgagaaataaaagacatacaaaaagaaaattta	3724		11
Qy 841	caacaacatttagatgcacaacacaaaaaattgataagacttaaaaacttcaacaaga	900		11
Db 3725	gaaccaaacccgagatgcacaacacaaaaaattgataagacttaaaaacttcaacaaga	3784		11
Qy 901	catggtatgattatcatttccttcgcgtgataattcttcataatcgtttgaagtgt	960		11
Db 3785	catggtatgattatcatttccttcgcgtgataattcttcataatcgtttgaagtgt	3844		11
Qy 961	tattcgcaggttgccacatgcatacgttatgcctacatgcgcgaagattgcattca	1020		11
Db 3845	tattcgcaggttgccacatgcatacgttatgcctacatgcgcgaagattgcattca	3904		11
Qy 1021	tggnaaatgataaactatgctttagaacatgataacggtataattttatgagtt	1080		11
Db 3905	tggnaaatgataaactatgctttagaacatgataacggtataattttatgagtt	3964		11
Qy 1081	agtgaggactccagttaaagacgctgaagatgtaggaagaaatttaagttcaaaaagcctat	1140		11
Db 3965	agtgaggactccagttaaagacgctgaagatgtaggaagaaatttaagttcaaaaagcctat	4024		11
Qy 1141	aatgcgactgttatatgaatcgtatgaggtattatcaagccaaactaataacatgatt	1200		11
Db 4025	gagtcgagatgtatgaatcgtatgaggtattatcaagccaaactaataacatgatt	4084		11
Qy 1201	gcaactatatacgcacttaaaaagttaagaataagattttttaccacccaattatct	1260		11
Db 4085	gcaactatatacgcacttaaaaagttaagaataagattttttaccacccaattatct	4140		11
Qy 1261	aattatgaaattcacagattca 1283			11
Db 4142	aattatgaaattcacagattca 4164			11
RESULT 3				
AAO78141	ID AAO78141 standard; DNA: 1257 BP.			
XX	AAO78141:			
AC	19-JUL-1995 (first entry)			
DT	XX			
XX	Staphylococcus epidermidis fema gene.			
DE	XX			
XX	fema protein; fema gene; methicillin-resistant bacteria; ds.			
XX	Staphylococcus epidermidis.			
OS	key			
XX	mat_peptide			
FT	1..1257			
XX	/*tag= a			
XX	EP625575-A.			
PN	23-NOV-1994.			
PD				

Fri Jun 21 08:38:19 2002

PI Gala J, Vannuffel P;
 XX WPI: 1999-287521/24.
 DR P-PSDB; AAY08215.
 DR New Staphylococcus-specific oligonucleotides
 PT Claim 15; Fig 6a-b; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 XX based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX Sequence 1305 BP; 513 A; 165 C; 222 G; 405 T; 0 other;
 SQ

Query Match 53.1%; Score 810.2; DB 20; Length 1305;
 Best Local Similarity 77.5%; Pred. No. 1.2e-149;
 Matches 994; Conservative 0; Mismatches 288; Indels 1; Gaps 1;

Qy 1 acagtaagaatttagcttactgatacaaatcccttactgacatttactcagatg 60
 Db 22 acagtcacagagtttggcaattatcacagataagatgcatatgcatcttccacaaatg 81
 Qy 61 gaaggtaattatgaactaaagtctgaaggtgacgattccatctcgttggaattaa 120
 Db 82 actgaataactatgagtgaaagttgcataataaaacagaactcacttcttggtataaa 141
 Qy 121 aataagaacacacagagtgatgagcagctgttttataactctgctgacatgaatga 180
 Db 142 aataagaatactgaggttattgacgctgacgtgttgacagcagtaaccagtcataatt 201
 Qy 181 tttaaatatttttactcaaatcgcgggcagtgattgattatcatataaagagctgtgt 240
 Db 202 tttaagtacttttattcaacggaggacctgttaattgattatgataatgagagctgtt 261
 Qy 241 cactttttttaaataagtaataatgataataaaagcataattgtcttttactaaga 300
 Db 262 cactttttttaaataagtaataatgataataaaagcataattgtcttttactaaga 321
 Qy 301 gtgacccctattctcttactcaatacttaacttaaatcagcgtgaaattattgaaatgt 360
 Db 322 gtgacccctatttaccataatcaataatttaataatcagtggtgaaattattgaaatgt 381
 Qy 361 ggcacatgattggttttcaataagatgagaattagattgaaacatgaagcgttttact 420
 Db 382 ggtaaatgattggttttcttataagatgagcactctcgttattgaaatgaagcgtttact 441
 Qy 421 aaaggttccatcttcttactcaatacttaacttaataatcagcgtgaaattattgaaatga 480
 Db 442 aaaggttctgacgtatcaataacacacagatacctcattctgttttagatttaaaataaa 501
 Qy 481 acggcttaagatgtactcaagaagatgagattgaagacgtaactactcaagaagta 540
 Db 502 acatctaaagatatataatggaatgagtagtctacgttaacgtaactcaaaaaagtt 561
 Qy 541 caaaaaatggttcaagtcgttccctatccgaagatgaattacacctattcttagatca 600
 Db 562 caaaaaatggttgaagtagtcttcttatacagaagaagacacttccatctccgttca 621
 Qy 601 ttatggaagatactacagaacgaagaggttgcgcgatagagatgattttctattat 660

Db 622 ttatggaagatacaaccgaaacgaagaattcccaagatagatgatagttcttattat 681
 Qy 661 aatcgattaaaaatactttaaagatagattatttagtaccattagcatattgacttcgat 720
 Db 682 aatcgctatagacatttcaaaagatcagtgctgttaccactagcttatataagttgat 741
 Qy 721 gagtatttgaagaacttaataatgaagagatgttcttataaagaatttaataaagcgt 780
 Db 742 gagtacatcgaaagattacaaaatgaacgtgaacatttaaaaagaagtgtaataaagt 801
 Qy 781 ctcaagatattgaagaagacgtgataataaagaagcttatacaaaaagaagataatt 840
 Db 802 ttaaaagtattgaaaaacgacacagacataaaaaggcatttataaaaagaatactt 861
 Qy 841 caacaacaatttagatgcgaatacaacaaaaaattgagagctcaaaaacttacaacaa 900
 Db 862 gaaaaacaatttagatcccaatcaacaaaaaattagagcgtcaaaaattacaacgaa 921
 Qy 901 catggaatgaattacatttctcagctggatatttcttcttattccatttgaagttgtt 960
 Db 922 catggaatgaattacatttctcagcaggttcttcttattccatttgaagttgtt 981
 Qy 961 tattacgaggtgacacatcgaaatcggttattctgctacatgcgcggaagttatgcaattca 1020
 Db 982 tattatgcaggtggaacttctataataatagacatttgcaggcagttatgctattcaa 1041
 Qy 1021 tggaataatgaactatgctttagaacatggaattaaacogttataatttttggagtt 1080
 Db 1042 tggacaatgatttaactatgcaattgatcatggttattgatatagatacaatttctatgtatt 1101
 Qy 1081 agtggggacttcagtgagacgtgagatgagatgtagtagtaattagttcaaaaaggctat 1140
 Db 1102 agcggtaatttttaggaagcgtgagatggtgagtcatttaataatttaaaaaggcttc 1161
 Qy 1141 aatgctgatttattgaattatgattgatttatttcaagcgaatcaataaactatgtat 1200
 Db 1162 aatgcagacgttaattgattgattggtgagacttggaaacctatttaaaagggttc 1221
 Qy 1201 gcaatctataacgcacttaaaagttaaaagaataatgattttttaccaccaactatct 1260
 Db 1222 tcagtgttaagacactcaaaaagattaa-aaaaagatttaattaaaggggaatagac 1280
 Qy 1261 aattatgaatttacagagtttaa 1283
 Db 1281 gaatatgaatttacagagtttaa 1303

RESULT 6
 AAX37804
 ID AAX37804 standard; DNA; 1342 BP.
 XX
 AC AAX37804;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus hominis FemA DNA.
 XX
 KW FemA; identification; detection; therapy; infection; femB;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus hominis.
 XX
 PH Key Location/Qualifiers
 XX CDS 64..1327
 XX FT /*tag= a
 XX FT /product= "FemA"
 XX
 PN WO9916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.
 XX

PR 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 XX Gala J, Vannuffel P;
 PI
 XX WPI: 1999-287521/24.
 DR P-PSDB: AAY08221.
 XX
 XX New Staphylococcus-specific oligonucleotides

PS Claim 27, Fig 12, 48pp; English.

XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown staphylococci species.
 CC Since the fema sequence is similar to the molecular genotyping of fema
 CC oligonucleotides can also be used for the molecular genotyping of fema
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 XX Sequence 1342 BP; 544 A; 161 C; 217 G; 420 T; 0 other;

Query Match 62.4%; Score 800.8; DB 20; Length 1342;
 Best Local Similarity 78.7%; Pred. No. 8,6e-148;
 Matches 969; Conservative 0; Mismatches 262; Indels 1; Gaps 1;

QY 1 acagctaagaattagtgcttactatgaatgaatgcttaccatttaccagatg 60
 DB 82 acagctaagaattagtgcttactatgaatgaatgcttaccatttaccagatg 141
 QY 61 gaagtaattatgaactaagtgctgaagtgacgattcaatcgttgaagtaaa 120
 DB 142 actgaataactagtgctgaagtgacgattcaatcgttgaagtaaa 200
 QY 121 aataatgacaacagtgatgacgatttactaatcgttgaagtaaa 180
 DB 201 aataatgacaacagtgatgacgatttactaatcgttgaagtaaa 260
 QY 181 tttaaatatttactcaaatcgcggaagtgatgatttgaataaagagctgtt 240
 DB 261 tttaaatatttactcaaatcgcggaagtgatgatttgaataaagagctgtt 320
 QY 241 cacttttcttaagtaagtaaatatgataaagaacataatgcttatacaga 300
 DB 321 cacttttcttaagtaagtaaatatgataaagaacataatgcttatacaga 380
 QY 301 gttgacctatcttactatcaatcaatcaatcaatcaatcaatcaatcaat 360
 DB 381 atagacctatcttactatcaatcaatcaatcaatcaatcaatcaatcaat 440
 QY 361 ggcagtgatgttttcaataagaatggaagtaagtgattggaacatgagcttcat 420
 DB 441 ggcagtgatgttttcaataagaatggaagtaagtgattggaacatgagcttcat 500
 QY 421 aaaggttccatctcttactaagaatggaatggaatggaatggaatggaatgga 480
 DB 501 aaaggttccatctcttactaagaatggaatggaatggaatggaatggaatgga 560
 QY 481 acggttaagaatgactcaagaagtaagtaagttgaagaagcgtaatacaagaagta 540
 DB 561 actgttaagaatgactcaagaagtaagtaagttgaagaagcgtaatacaagaagta 620
 QY 541 caaaaaatggtcgaagtcggttccatccggaatgaatattactatcttataatca 600

DB 621 caaaaaatggtcgaagtcggttccatccggaatgaatattactatccatccagatca 680
 QY 601 tttaatggaatgactcaagaagtaagtgctcggaatggaatggaatggaatggaat 660
 DB 681 tttaatggaatgactcaagaagtaagtgctcggaatggaatggaatggaatggaat 740
 QY 661 aatgcttaaaatgactcaagaatggaatggaatggaatggaatggaatggaatgga 720
 DB 741 aatgcttaaaatgactcaagaatggaatggaatggaatggaatggaatggaatgga 800
 QY 721 gactatggaatgactcaagaatggaatggaatggaatggaatggaatggaatgga 780
 DB 801 gactatggaatgactcaagaatggaatggaatggaatggaatggaatggaatgga 860
 QY 781 ctcaagaatgactcaagaatggaatggaatggaatggaatggaatggaatggaatgga 840
 DB 861 ctcaagaatgactcaagaatggaatggaatggaatggaatggaatggaatggaatgga 920
 QY 841 caacacaaatgactcaagaatggaatggaatggaatggaatggaatggaatggaatgga 900
 DB 921 gaacacaaatgactcaagaatggaatggaatggaatggaatggaatggaatggaatgga 980
 QY 901 catggaatgactcaagaatggaatggaatggaatggaatggaatggaatggaatgga 960
 DB 981 catggaatgactcaagaatggaatggaatggaatggaatggaatggaatggaatgga 1040
 QY 961 tathacagagtgacatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgat 1020
 DB 1041 tathacagagtgacatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgat 1100
 QY 1021 tggaaatgataactatgcttgaacatggaatggaatggaatggaatggaatggaatgga 1080
 DB 1101 tggaaatgataactatgcttgaacatggaatggaatggaatggaatggaatggaatgga 1160
 QY 1081 agtggagactcgatggaatggaatggaatggaatggaatggaatggaatggaatgga 1140
 DB 1161 agtggagactcgatggaatggaatggaatggaatggaatggaatggaatggaatgga 1220
 QY 1141 aatggaatgataactatgcttgaacatggaatggaatggaatggaatggaatggaatgga 1200
 DB 1221 aatggaatgataactatgcttgaacatggaatggaatggaatggaatggaatggaatgga 1280
 QY 1201 gcaatctataacgacttaaaagtaagaa 1232
 DB 1281 tcaatctataacgacttaaaagtaagaa 1312

RESULT 7
 AAX37800
 ID AAX37800 standard; DNM; 1295 BP.
 XX
 AC AAX37800;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus xylosus Fema DNA.
 XX
 KW Fema; identification; detection; therapy; infection; fema;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus xylosus.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..1295
 FT /tag= a
 FT /product= "Fema"
 FT /note= "partial sequence, no start or stop codon"
 XX
 PD W09916780-A2.
 XX
 PD 08-APR-1999.

PF 28-SEP-1998; 98WO-BE00141.
 XX
 PR 26-SEP-1997; 97EP-0870146.
 XX
 (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX
 DR WPI; 1999-287521/24.
 DR P-PSDB; AAY08217.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 19; Fig 8a-b; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 1295 BP; 511 A; 156 C; 243 G; 385 T; 0 other;

Query Match 58.4%; Score 749.6; DB 20; Length 1295;
 Best Local Similarity 74.8%; Pred. No. 9e-138;
 Matches 957; Conservative 0; Mismatches 314; Indels 9; Gaps 1;

QY 13 tttagtgaatttactgacaaatgctttagcatttttactcagatggaagttaatt 72
 DB 13 ttgggtgcaatttcagataaaagcgaatagcatttcagcaaatgtagggaatt 72
 QY 73 gaactaaagtgtggaagtgacgattccatctcgttaggaattaaataatgacaa 132
 DB 73 gaattgaaatgcgaagtgactgaaacacatttagtgattataaaacaaatgata 132
 QY 133 caagtgtgagatgttttaactgtgtacgtgtacgtgaatgaaatttttaacttt 192
 DB 133 gaagtgtgagatgttttaactgtgtacgtgtacgtgaatgaaatttttaacttt 192
 QY 193 tactcaaatcgccgagtgattgattgataaaagagctgttcactttttttt 252
 DB 193 tatataatgagggccggttatagattttgaaataaagattgagcattttttc 252
 QY 253 aatgaataatgataatgtataaaagcattttgttttttctaaagagcttccat 312
 DB 253 aatgaactatcatttaattgtgaaacacataatgcttttttttaagagtgatcct 312
 QY 313 ctctctataacttaacttaactgacggtgaaattattggaatgctggccatgattg 372
 DB 313 ttgacatacaatcaccgaatcattggtgaggtattggaaatgaggaacatgatgg 372
 QY 373 tttttcaaatgaggaattgattgacatgaggtcttctcaaaagcttccat 432
 DB 373 attttcgataaataagcagcttggatacaaacaccagaggttttaactggttcgat 432
 QY 433 cctatctcaagaatgatactattcattcagtttttagatttaaaagataaaacggctaaagt 492
 DB 433 tcaatttcaaatgattgttcactctgactggtatttaggtgaaactgctaaagt 492
 QY 493 gtactcaaaaggaatgattgataaaagcgtcaataactaagaagaataaaatggt 552
 DB 493 gtactcaaaatggtatgatttaccgtaaacgtaactataaaagtcataaaatggc 552

QY 553 gtcaagtcgctttcttactcgaagatgaattacctatctttagatcatattatggagat 612
 DB 553 gtgaagtgaaaggttcttaaggaagatgagttgccaattttccgttcattcattggaagat 612
 QY 613 actacgaaacgaagagttcgccgataagatgagttttctattataatcattcaaaa 672
 DB 613 acatctgaaactaaagaccttgacgataagacgagtggttttactacaatagataagg 672
 QY 673 tacttaagatagaggtatttagtaccattagcatatgttgacttgatgagatattgaa 732
 DB 673 tattataagatcgctgatttagtaccctagcttattgatttcaatgaatattgaa 732
 QY 733 gaacttaataatgaaagaggtgtttcttaataaagatttaataaaggcgctcaagatt 792
 DB 733 gaattgcaagctgaaaggtggttgaagcaagatcatcaataaagcagtaaaagatc 792
 QY 793 gagaagagacctgataataaagaagcttatacaaaagagataatcttcaacaacatta 852
 DB 793 gagaagagacctgataataaagaagcttatacaaaagagataatctagagaaacatt 852
 QY 853 gatgcaatacaaaatgatgaagctaaacacttacaacagaacatggttaagaa 912
 DB 853 atagcgaatcaaaatgatgaagctaaacacttacaacagaacatggttaagaa 912
 QY 913 ttactatttcagctggtatttttcttcaataatccgtttgaggtgtttattacgaggt 972
 DB 913 ctaccaatctcagcagcatattctcatcattaaaccttgaagtagtgtattatcggt 972
 QY 973 ggcacatcgatgttctatcgtcactatgccggaagttatgcaattcaatgaaatgata 1032
 DB 973 ggaagctcaaatgatttagacatttctggtgattgcttccatcaatggaagatt 1032
 QY 1033 aactatctttagaacatggaattaaacgtttataattttttaggttagtgggacttc 1092
 DB 1033 aactatctttgaccataatattgatgataataattttttaggaattagtggtcattt 1092
 QY 1093 agtgaagcctgaagatgagtaggaattaaagttcaaaaaagcgtataatgcgtgatt 1152
 DB 1093 acagagatgagagatgagcgggtgatttaattaaaaaaggatttaattcgagtgta 1152
 QY 1153 attgaatagtaggtgatttttctatcaagcccaatcaataaacctatgtagtcaactat 1209
 DB 1153 ggggaatagtggtgatttttataaaccatcaataaaccatgatacaaaatttatacy 1212
 QY 1210 -----aacgcacttaaaagttaaagaataatgattttttaccacccaatttctaat 1263
 DB 1213 acattaaagaaataaagataaaagaaataaacatttaataagaagggaactaagctag 1272
 QY 1264 tatgaattttacagagttaa 1283
 DB 1273 aatgaattttacagagttaa 1292

RESULT 8
 AAX37805
 ID AAX37805 standard; DNA; 1371 BP.
 XX
 AC AAX37805;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Staphylococcus saprophyticus FemA DNA.
 XX
 KW FemA; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Staphylococcus saprophyticus.
 XX
 FH Key Location/Qualifiers
 FT CDS 64..1326
 FT /*tag= a
 FT /product= "FemA"

XX MO9916780-A2.
 XX 08-APR-1999.
 XX 28-SEP-1998; 98WO-BE00141.
 XX 26-SEP-1997; 97EP-0870146.
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 XX (UTLO-) UNIV CATHOLIQUE LOUVAIN.
 PI Gala J, Vannuffel P;
 DR WPI: 1999-287521/24.
 DR P-PSDB: AAY08222.
 XX New Staphylococcus-specific oligonucleotides
 PT Claim 29; Fig 13; 48pp; English.
 XX This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus fema nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various fema
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the fema sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The fema nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the fema
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 XX Sequence 1371 BP; 545 A; 155 C; 248 G; 423 T; 0 other:
 SQ
 Query Match 57.8%; Score 741.2; DB 20; Length 1371;
 Best Local Similarity 73.6%; Pred. No. 4e-136;
 Matches 944; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

Db 502 actggtttaccaccacttcaataaagattccattcgttttagattagctgggaaa 561
 QY 481 acggttaagatgtactcaaaaggatgatagtttaagaagcgtaactaagaagta 540
 Db 562 actgttaagacgtacttaattgatagtatgtttacgttaacgaaatacaaaagaa 621
 QY 541 caaaaaatgtgtcaaatgtccgtttccatcgcgaagatgaattaccattcttagata 600
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 Db 862 gtcaagatatagaaaaaagacagaataaataaagaagctataaagaataattta 921
 QY 841 caacacaaattagatgcaaatcaacaaataattgtgtaagcttaaaacttaacaaga 900
 Db 922 gaacacaaactgattgcaaacacaaataaataagataagccactgcttaacaagaag 981
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 Db 1342 aactaagctagaatgaatttta 1363

RESULT 9
 AAX37799 standard; DNA; 1280 BP.
 ID AAX37799
 XX AAX37799;
 AC
 XX 09-JUN-1999 (first entry)
 DT
 XX Staphylococcus lugdunensis Fema DNA.
 DE
 XX Fema; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX Staphylococcus lugdunensis.

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XX
FH Key Location/Qualifiers
FT CDS 1..1280
FT /tag= "femA"
FT /product= "partial sequence, no start or stop codon"
XX
XX W09916780-A2.
PN
PN
PD 08-APR-1999.
XX
XX 28-SEP-1998; 98WO-BE00141.
PF
XX
XX 26-SEP-1997; 97EP-0870146.
PR
XX
XX (BENA-) BELGIAN MIN NAT DEFENCE.
PA
XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.
PI
XX Gala J. Vannuffel P;
XX
XX WPI; 1999-287521/24.
DR
XX P-PSDB; AAY08216.
DR
XX
XX New Staphylococcus-specific oligonucleotides
FT
XX
XX Claim 17; Fig 7a-b; 48pp; English.
XX
XX This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.
XX
XX Sequence 1280 BP; 484 A; 197 G; 221 C; 378 T; 0 other;
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Query Match 57.4%; Score 736.6; DB 20; Length 1280;
Best Local Similarity 74.0%; Pred. No. 3.1e-135;
Matches 949; Conservative 0; Mismatches 329; Indels 5; Gaps 1;

QY 1 acagctaaagaatttagtgactttactgatcaaatgcttatgcatttactcagatg 60
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QY 61 gaaggtaattgaacttaaagttgctgaaggtacggtaccatctcgttaggaattaaa 120
Db 61 acagdtgaactatacttaattaaaaagttgccgaaaaaacagacaacatttagttggtttaa 120

QY 121 aataatgacaccaagtgattgcagcatgttttattaactcgtctacctgtaataaaat 180
Db 121 aataataacaggaagtaatgcagcatgttttattgacagctgaccagcatgaagttt 180

QY 181 tttaaatattttactcaaacctcgggccagtgattgatgatataaagaagcttcgtt 240
Db 181 tttaaatattttcacgcaatagaggcccagttatagattatgctaaccaagaactigta 240

QY 241 cactttttctttaatgaataaagtataatgtataaaagcataatgtgtttttactaaga 300
Db 241 cattttttctttaatgagtaactaaatattttaaaaaagtataactgtctcatgcgcg 300

QY 301 gttgaccttatcttcctatccaacttaacttaactgacggtggaattatttgtgaatgct 360
Db 301 atagatccacttacttactatccaatagagaccatgcggttaatatataacggcgaatgct 360

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Fri Jun 21 08:38:19 2002

Staphylococcus schleiferi FemA DNA.
FemA; identification; detection; therapy; infection; femB;
amplification; genotyping; gram-positive bacteria; vaccine; ss.
Staphylococcus schleiferi.
Key Location/Qualifiers
CDS 1..1297
/tag- a
/product- "FemA"
/note- "partial sequence, no start or stop codon"
XX WO9916780-A2.
XX 08-APR-1999.
XX 28-SEP-1998; 98WO-BE00141.
XX 26-SEP-1997; 97EP-0870146.
XX (BENA-) BELGIAN MIN NAT DEFENCE.
XX (UULO-) UNIV CATHOLIQUE LOUVAIN.
XX Gala J, Vannuffel P;
XX WPI; 1999-287521/24.
XX P-PSDB; AAY08219.
XX New Staphylococcus-specific oligonucleotides
XX Claim 23; Flg 10a-b; 48pp; English.
XX This invention describes novel Staphylococcus-specific oligonucleotides
XX based on the consensus femA nucleotide sequence which are used to
XX develop products for the identification, detection and therapy of
XX infections. The oligonucleotides can be used for the genetic
XX amplification, the identification and/or quantification of various femA
XX sequences which are specific to known or unknown Staphylococci species.
XX Since the femA sequence is similar to the femB sequence, the
XX oligonucleotides can also be used for the molecular genotyping of femB
XX genes of different Staphylococci species or other gram-positive bacteria.
XX The femA nucleic acids can also be used in therapeutic applications.
XX They can also be used to identify inhibitors, e.g. antibodies or
XX antisense oligonucleotides, for blocking expression of the femA
XX nucleotide sequences. They can also be used for producing vaccines
XX against Staphylococci infections.
XX Sequence 1297 BP; 495 A; 184 C; 249 G; 369 T; 0 other;

Query Match 52.3%; Score 670.6; DB 20; Length 1297;
Best Local Similarity 71.6%; Pred. No. 2.6e-122;
Matches 880; Conservative 0; Mismatches 349; Indels 0; Gaps 0;

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QY 70 tatgaacttaagtgtgtagcgaggttcacatctctaggaataaataatgac 129
DB 70 tatgaacttaagtgtgtagcgaggtttgaaacacatctctggtgcaataaagatacaac 129
QY 130 aacaaagtattgcagcatgtttatcaactgctgtacgtgtaataaataatgaaat 189
DB 130 aataacgtactgacgcatgtttactgacagcgaggtgcagtaataagtttttaatat 189
QY 190 ttttactcaaatcgccgagcagtgattgattatgataaagaagctgttcacttttc 249
DB 190 ttttattcaaccgagccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 249
QY 250 tttatgaattaagtaataatgtataaaagcataatgtctttatctaaaggtgacct 309

RESULT 12
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ID AAX37803 standard; DNA; 1284 BP.
XX
XX AAX37803;
AC

Fri Jun 21 08:38:19 2002

QY 539 tacaaaaaatggtgtcaaatccggttt 566
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Db 31 TAAAAAGGAATGGTTAAAGTAAGTTT 4

Search completed: June 20, 2002, 14:46:22
Job time: 18772 sec

PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
PI Rosen CA;
XX WPI; 1997-374922/35.
XX Polynucleotide(s) and proteins derived from *Staphylococcus aureus*
PT stored on computer readable medium and used in the production of
PT anti-*S.aureus* vaccines
XX
XX Claim 1; Page 1339-1340; 3271pp; English.

This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the *S.aureus* DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against *S.aureus* infection. The polypeptides can also be used in a kit for the immunodetection of *S.aureus* in a sample. *S.aureus* is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the *S.aureus* DNA sequences contained on the computer readable medium.

Sequence 3271 BP; 948 A; 625 C; 461 G; 1168 T; 69 other;

Query Match 25.48; Score 326; DB 18; Length 3271;
Best Local Similarity 75.5%; Pred. No. 8.2e-55;
Matches 429; Conservative 0; Mismatches 137; Indels 2; Gaps 2;

QY 1 acagctaaagaatttagtgacttactgacataaagcttccttagccattttactcagatg 60
| | | | | | | | | | | | | | | | | |
Db 571 ACAGCTAAAGAGTTTGGTGGCTTTACAGATAGCATGCCATACAGTCATTCACGCAAACT 512
| | | | | | | | | | | | | | | | | |
QY 61 gaaggttaattgaactaaagtgtgctgaaggtacggtacacatcctcgtaggaaataa 120
| | | | | | | | | | | | | | | | | |
Db 511 GTTGGCCACATATGAGTTAAAGTGTCTGAAGGTTATGAAACACATTTAGTGGGAATAAAA 452
| | | | | | | | | | | | | | | | | |
QY 121 aataatgacacacacagtgatgacgcatgttttaataactgctgacgtgaatgaaatt 180
| | | | | | | | | | | | | | | | | |
Db 451 AACAAATAAACGAGGTCATTCAGCTTGCTTACTGCTGTACCTGTGTATGAAGTG 392
| | | | | | | | | | | | | | | | | |
QY 181 tttaaatattttactcaaatcgccgagtgatgattatgataataaagagctgttt 240
| | | | | | | | | | | | | | | | | |
Db 391 TTCAGATATTTTATTCAATCGCGTCCAGTGATGTGATTGTAATCAAGAACCTGTA 332
| | | | | | | | | | | | | | | | | |
QY 241 cacttttctttaaataagtaataatgtaaaaaagcataattgtctttatcttaaga 300
| | | | | | | | | | | | | | | | | |
Db 331 CACTTTTCTTAAATGATATCAAAATATGTTAAAAACATCGTGTCTATACCTACAT 272
| | | | | | | | | | | | | | | | | |
QY 301 gttgaccttattcttcttcaataactaataatcaatgacggggaattatggaaatgct 360
| | | | | | | | | | | | | | | | | |
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Db 91 ACAGCAGATGACATCAATAAAAAATATGGATGGACTTAAGNAAANGAACACCAAAAAAGT 32

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us-09-509-234c-46.rng

Page 17

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us-09-509-234c-46.rn1

Page 1

GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: June 20, 2002, 12:03:54 ; Search time 208.59 Seconds
(without alignments)
1510.848 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	277.2	21.6	453	3	US-08-714-918-9 Sequence 9, Appl
3	277.2	21.6	453	4	US-09-265-315-9 Sequence 9, Appl
4	277.2	21.6	453	4	US-09-265-315-9 Sequence 9, Appl
5	277.2	21.6	453	4	US-09-266-417-9 Sequence 6, Appl
6	236	20.0	410	3	US-08-714-918-6 Sequence 6, Appl
7	236	20.0	410	4	US-09-265-315-6 Sequence 6, Appl
8	256	20.0	410	4	US-09-266-417-6 Sequence 6, Appl
9	256	20.0	410	4	US-08-714-918-4 Sequence 4, Appl
10	221.2	17.2	400	3	US-09-265-315-4 Sequence 4, Appl
11	221.2	17.2	400	4	US-09-265-315-4 Sequence 4, Appl
12	221.2	17.2	400	4	US-09-266-417-4 Sequence 4, Appl
13	221.2	17.2	400	4	US-08-714-918-19 Sequence 19, Appl
14	97.6	7.6	5253	3	US-08-265-315-19 Sequence 19, Appl
15	97.6	7.6	5253	4	US-09-265-315-19 Sequence 19, Appl
16	97.6	7.6	5253	4	US-09-266-417-19 Sequence 19, Appl
17	97.6	7.6	5253	4	US-08-714-918-14 Sequence 14, Appl
18	56.2	4.4	8920	2	US-08-446-855A-1 Sequence 1, Appl
19	56.2	4.4	8920	4	US-08-446-855A-1 Sequence 1, Appl
20	56.2	4.4	8920	4	US-09-150-741-1 Sequence 1, Appl
21	55.6	4.3	930	4	US-08-936-165A-74 Sequence 74, Appl
22	54.6	4.3	658	4	US-08-998-416-595 Sequence 595, App
23	51.8	4.0	615	4	US-08-998-416-186 Sequence 2, Appl
24	51.8	4.0	5361	4	US-08-973-462-2 Sequence 2, Appl
25	51.8	4.0	6152	4	US-08-973-462-1 Sequence 2, Appl
26	51	4.0	1431	4	US-09-316-083-2 Sequence 13, Appl
27	51	4.0	19124	2	US-08-487-826B-13 Sequence 13, Appl

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c	33	48	3.7	3095	6	5231168-1	Patent No. 5231168
c	34	47.8	3.7	636	4	US-08-998-416-1137	Sequence 288, App
c	35	47.2	3.7	837	4	US-08-998-416-288	Sequence 10, Appl
c	36	47.2	3.7	4766	5	PCT-US93-07261-10	Sequence 1, Appl
c	37	45.4	3.5	9636	1	US-08-323-170B-1	Sequence 1137, Ap
c	38	45.4	3.5	9636	4	US-08-954-441-1	Sequence 1, Appl
c	39	44	3.4	636	4	US-08-998-416-1137	Sequence 186, App
c	40	44	3.4	1956	4	US-08-998-416-186	Sequence 1, Appl
c	41	43.8	3.4	615	4	US-08-998-416-186	Sequence 1, Appl
c	42	43.8	3.4	6243	2	US-09-056-075-1	Sequence 1, Appl
c	43	43.6	3.4	634	1	US-08-450-065-1	Sequence 1, Appl
c	44	43.6	3.4	634	1	US-08-450-065-1	Sequence 1, Appl
c	45	43.4	3.4	724	4	US-08-998-416-683	Sequence 683, App

ALIGNMENTS

RESULT 1
US-08-330-154-1
Sequence 1, Application US/08330154
Patent No. 5587307
GENERAL INFORMATION:
APPLICANT: Alborn Jr., William E
APPLICANT: Hoskins, Joann
APPLICANT: Skatrud, Paul L
APPLICANT: Unal, Serhat
TITLE OF INVENTION: FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS.
TITLE OF INVENTION: FEMA PROTEIN, AND VECTORS AND MICROORGANISMS COMPRISING
TITLE OF INVENTION: THE FEMA GENE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Division/ARH
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,154
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/208,925
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US/08/057,163
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Amy E
REGISTRATION NUMBER: 33,894
REFERENCE/DOCKET NUMBER: X-8894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3169
TELEFAX: 317-276-1284
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

Fri Jun 21 08:38:19 2002

LOCATION: 1..1257
US-08-330-154-1

Query Match 68.38; Score 876.2; DB 1; Length 1257;
Best Local Similarity 81.98; Pred. No. 3.5e-190;
Matches 1010; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

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QY 181 tttaaatattttactcaaatcgcggccagtgattgattgattgataataaagagctgtt 240
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QY 241 cactttttctttaaagtaataatgataaagcctttaaagccttcttcttcttaaga 300
DB 265 CATTTTTCCTTAATGAATGAGTAAATATGTAATAAATAATATATTTTATTTAAGA 324
QY 301 gttgaccttacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 360
DB 325 GTTGACCAATACCTTCCATATCAATATTAATCATGAGGAGAAATACCTGGAATGCA 384
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DB 385 GGTCAATGATGTTGATGAATTTAGAGAGTTAGAGATATTAACACAGAGGATCCAC 444
QY 421 aaagctccctcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 480
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DB 685 AACAGATTTCAACATTAATAAGACCGCTGTTTATGACACAGCTAGCTATATTAAC 744
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QY 841 caacaaatattgagatgcaaatcaacaaatgagtgatgagtgatgagtgatgagtg 900
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QY 961 tattacgcaggtggcacatcgaaatcttcttcttcttcttcttcttcttcttctt 1020

DB 985 TACTACGCTGTGGAACCTTCAATCGTTTATCCCATTTTGCAGGAGCTATCGGTTCAA 1044
QY 1021 tggaaaaatgataaactatgcttttagaacaatggaaattaaacggttataattttatgagtt 1080
DB 1045 TGAAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1104
QY 1081 agtgggagcttcagtgaaagcgtgaaagatgtaggagtaattaaagttcaaaaaagcctat 1140
DB 1105 AGTGGTGACTTTAGTGAAGATGCTGAAGATGCTGGCGTAGTTAAGTTTAAAAAGGCTAT 1164
QY 1141 aatgctgattgttattgattgattgattgattgattgattgattgattgattgattgatt 1200
DB 1165 GATGCCGATGTTATAGATACGTTGGTGACTTTATTAACCTTATTAATTAACCAATGAT 1224
QY 1201 gcaatctataacgcacttaaaagttaaagaaa 1233
DB 1225 AACATTTATAGAACAACCTTAAAAAATAAAGAA 1257

RESULT 2
US-08-714-918-9
; Sequence 9, Application US/08714918
; Patent No. 6037123
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
; TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,918
; FILING DATE: September 13, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-714-918-9

Query Match 21.6%; Score 277.2; DB 3; Length 453;
Best Local Similarity 74.3%; Pred. No. 1.7e-54;
Matches 336; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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QY 667 ttaaaactcttaaaagatagatattagaccattagcatatgttacttgatgagat 726
DB 2 TTTAAATATTTACAAAGACGCTGTGTAACCTTACGATATATCACTTTAATGAATAT 61
QY 727 atgaagaacttaataatgaagatgtcttcaataaagattcaaaagcgctcaa 786
DB 62 ATTAAGAACTAAACGAAGCGGTGATTTTAAATAAAGATTAAAGCGCTTAAAG 121
QY 787 gatattgagaagagactgataataaagacttatataaagaagataactctcaaca 846
DB 122 GATATTGAAAAACGCTCTGTAATAAAGACATTAACACGAGATTAACCTTAAACAA 181
QY 847 caattagatgcaaatcaaaaataattgatgaagctaaactcaacaagaacatggt 906
DB 182 CAACCTTATCAAAATGAGCAAAAGATTGANCAGGTAACGCTTACAGANGANCATGCT 241
QY 907 aatgaattaccatttcacgttgatattcttcattcaatccgtttgaagttgattac 966
DB 242 AATGTTTACCTATCTCTCTGCTTCTCCTTATCAACGCTTGAANGTGTATTATAT 301
QY 967 gcaggtggcacatcgatcgctacactatgacggaagttatgcaattcaatgaaa 1026
DB 302 GCTGTGCTGATCAATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
QY 1027 atgtaaacatctctttagaagactgaagtaaacgttataattttatggaagttatg 1086
DB 362 ATGTTATTTTTCATTAATATCATATGCGATTTCGCTTATTAATTTTCTATGCTGT 421
QY 1087 gacttcagtgaaagcgtgaagatgtagagt 1118
DB 422 NAATTTCAGNAGGTGCTGTAAGATGCTGCTGT 453
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RESULT 3
US-09-265-315-9
Sequence 9, Application US/09265315
Patent No. 6187541

GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-265-315-9

Query Match 21.6%; Score 277.2; DB 4; Length 453;
Best Local Similarity 74.3%; Pred. No. 1.7e-54;
Matches 336; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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QY 667 ttaaaactcttaaaagatagatattagaccattagcatatgttacttgatgagat 726
DB 2 TTTAAATATTTACAAAGACGCTGTGTAACCTTACGATATATCACTTTAATGAATAT 61
QY 727 atgaagaacttaataatgaagatgtcttcaataaagattcaaaagcgctcaa 786
DB 62 ATTAAGAACTAAACGAAGCGGTGATTTTAAATAAAGATTAAAGCGCTTAAAG 121
QY 787 gatattgagaagagactgataataaagacttataaagaagatacttcaaca 846
DB 122 GATATTGAAAAACGCTCTGTAATAAAGACATTAACAGGAGATTAACCTTAAACAA 181
QY 847 caattagatgcaaatcaaaaataattgatgaagctaaactcaacaagaacatggt 906
DB 182 CAACCTTATCAAAATGAGCAAAAGATTGANCAGGTAACGCTTACAGANGANCATGCT 241
QY 907 aatgaattaccatttcacgttgatattcttcattcaatccgtttgaagttgattac 966
DB 242 AATGTTTACCTATCTCTCTGCTTCTCCTTATCAACGCTTGAANGTGTATTATAT 301
QY 967 gcaggtggcacatcgatcgctacactatgacggaagttatgcaattcaatgaaa 1026
DB 302 GCTGTGCTGATCAATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
QY 1027 atgtaaacatctctttagaagactgaagtaaacgttataattttatggaagttatg 1086
DB 362 ATGTTATTTTTCATTAATATCATATGCGATTTCGCTTATTAATTTTCTATGCTGT 421
QY 1087 gacttcagtgaaagcgtgaagatgtagagt 1118
DB 422 NAATTTCAGNAGGTGCTGTAAGATGCTGCTGT 453
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RESULT 4

US-09-265-315-9

Sequence 9, Application US/09265315

Patent No. 6187541

GENERAL INFORMATION:

APPLICANT: Benton, Bret

APPLICANT: Lee, Ying J.

APPLICANT: Malouin, Francois

APPLICANT: Martin, Patrick K.

APPLICANT: Schmid, Molly B.

APPLICANT: Sun, Dongxu

TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

TITLE OF INVENTION: TARGET GENES

Fri Jun 21 08:38:19 2002

362 ATGNTAATTTTGCATTAATCATGCGATTGCGTATATTAATNCTATGCTGTAGTGGT 421

1087 gacttcagtgagacgctgagatgtagagat 1118

422 NAATTTCAGNAGGCTGCTGAAGATGCTGGTGT 453

RESULT 5

US-09-266-417-9

; Sequence 9, Application US/09266417

; Patent No. 6228588

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/266,417

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 240/248

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 453 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-266-417-9

Query Match 21.6%; Score 277.2; DB 4; Length 453;

Best Local Similarity 74.3%; Pred. No. 1.7e-54;

Matches 336; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

667 ttaaaactttaaagatagatttagtaccattagctattgacttcgtagtat 726

2 TTAATAATTACAAAGCGGTGTGTGTTAGTACCTTNGCGTATATCAACTTTAATGAATAT 61

727 attgaagaacttaataagaagatgttcttctaataagatttaataaaggcgctcaaa 786

62 ATTAAGAAGCTAAACGAGCGGTGATATTTTAAATAAAGATTTAAATAAAGCGTTAAAG 121

787 gatattgagaagcgactgataaagaagccttatacaaaagagataaacttctcaacaa 846

122 GATATTGAAAGAGCTCTGAAATAAAGACACATCAACGAGATTAATTACACAA 181

847 caattagatgcaatacaaaaatttgaagcttaaaaaacttacacaagaacatggt 906

182 CAACGTGATGCAATATGCAAAAGATTGANGACGGTTAACCGTCTACAGANGANCATGGT 241

907 aatgaattacatttcagctggatatttcttctaataatccgtttgaagttgtttattac 966

242 ATGNTTTACCTATCTCTCTGTTCTCTCTTTTATCAATCCNTTTTGANGTTGTTTATAT 301

967 gcaggtggcaactcgaatcgttatcgtcactatccggaagttatgcaattcaatgaa 1026

302 GCTGTGGTGTACATCAAAATGNTTCCGTCATTTTCCGGGANGTTATGCGTGCATGGAA 361

1027 atgataaactatgcttttagacatggaatttaacccgtttataatttttaggagttagtg 1086

Query Match 21.6%; Score 277.2; DB 4; Length 453;

Best Local Similarity 74.3%; Pred. No. 1.7e-54;

Matches 336; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

667 ttaaaactttaaagatagatttagtaccattagctattgacttcgtagtat 726

2 TTAATAATTACAAAGCGGTGTGTGTTAGTACCTTNGCGTATATCAACTTTAATGAATAT 61

727 attgaagaacttaataagaagatgttcttctaataagatttaataaaggcgctcaaa 786

62 ATTAAGAAGCTAAACGAGCGGTGATATTTTAAATAAAGATTTAAATAAAGCGTTAAAG 121

787 gatattgagaagcgactgataaagaagccttatacaaaagagataaacttctcaacaa 846

122 GATATTGAAAGAGCTCTGAAATAAAGACACATCAACGAGATTAATTACACAA 181

847 caattagatgcaatacaaaaatttgaagcttaaaaaacttacacaagaacatggt 906

182 CAACGTGATGCAATATGCAAAAGATTGANGACGGTTAACCGTCTACAGANGANCATGGT 241

907 aatgaattacatttcagctggatatttcttctaataatccgtttgaagttgtttattac 966

242 ATGNTTTACCTATCTCTCTGTTCTCTCTTTTATCAATCCNTTTTGANGTTGTTTATAT 301

967 gcaggtggcaactcgaatcgttatcgtcactatccggaagttatgcaattcaatgaa 1026

302 GCTGTGGTGTACATCAAAATGNTTCCGTCATTTTCCGGGANGTTATGCGTGCATGGAA 361

1027 atgataaactatgcttttagacatggaatttaacccgtttataatttttaggagttagtg 1086

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DB 62 ATTAAGAACTAAAGAGACCGTGATATTTTAAATAAGATTAAAGCGTTAAAG 121
QY 787 gatattgagaagacccgtgataaagaagccttaacaaagaagatacttcaacaa 846
DB 122 GATATTGAAAAACGTCTGAAAAATMAAAAGCACATAACGCGAGTAACCTACACAA 181
QY 847 caattagatgcaaacacaaataattgtagaagctaaactacacagaacatggt 906
DB 182 CAAGCTGATGCAAAATGACCAAAATGATGAGACGTAACGCTACAAAGNAGCATGGT 241
QY 907 aatgaattaccatttcagctgatacttctcattcaatccgtttgaagttgttacc 966
DB 242 AATGNTTACCTATCTCTCCGTTTCTCCTTATCAATCCNTTGAAGTTGTTATAT 301
QY 967 gcaggtgagacatcgatcgttactcgtcactatgcgggaagtatgcaatcgaatg 1026
DB 302 GCGTGTGATACATCAAAATGCMTCCTGATTTTCCGAGNCTTATGCGTCAATGGGA 361
QY 1027 atgataactatgctttagaacaatggaatcaaccgttataattttatgagttag 1086
DB 362 ATGTTAAATTGTCATTAATCAATGCGATTGCGGTTATTAATNCTATGCTTAGTGT 421
QY 1087 gacttcagtgagaagcgtcgaagatgtagagt 1118
DB 422 NAATTTCAGNAGGTGCTGAGATGCTGTGT 453

RESULT 6
US-08-714-918-6
; Sequence 6, Application US/08714918
; Patent No. 6037123
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714, 918
; FILING DATE: September 13, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Waidburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-714-918-6

Query Match      20.0%; Score 256; DB 3; Length 410;
Best Local Similarity 76.2%; Pred. No. 1.1e-49;
Matches 310; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

DB 644 atgtagttcttataatcgtatgaataaacttaagaatgagtagttaccattag 703
QY 644 atgtagttcttataatcgtatgaataaacttaagaatgagtagttaccattag 703
DB 4 ATGCAAAATWTAATCAATGCTTAAATATTACAAAGACCGTGTGACTGCTTTAG 63
QY 704 catatgtgactcgtatgagatattgagaacttaataatgaagatgttcttaata 763
DB 64 CGTATATCACTTTAATGATATATTTAAAGACTAAACGAAGCGTATTTTAAAT 123
QY 764 aagatttaaatgaagcgtcaaatatgagaagagactgataataagaagcttata 823
DB 124 AAGATTAAATTAAGCGTTAAAGATATGATAAAGCTCTGAAAATAAAGACACATA 183
QY 824 acaaaagagataatcttcaacacaaatagatgcaaatcaacaaaaattgataagcta 883
DB 184 ACAAGCGATFACTTACACACAACTTGAATGCAATGACAAATGAGCAAGATGAAGAT 243
QY 884 aaacttacaacaagaacatggtatgaatcttaccatttcagctgagattcttcata 943
DB 244 AACGCTACAAAGANGAACATGCTATGATTAATCTCTGCTGCTTCTTCTTATGCA 303
QY 944 atcgtttgaagtgtttattttagcaggtgacatcgatcgtatcgtacatgacg 1003
DB 304 ATCCATTTGANGTGTGTTATATGCTGCTGATGATCAATTAATGATTCGCTATTTCCG 363
QY 1004 gaagtagatcaatcaatggaataatgataaactatgctttagaagat 1050
DB 364 GAAGTTATGCGTGCATATGGAAATGATTATATGATTAATATCAT 410

RESULT 7
US-09-265-315-6
; Sequence 6, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265, 315

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RESULT 8
US-09-265-315-6
; Sequence 6, Application US/09465315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTION ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES

Qy	644	atgatgtttctattataatcagattaaatactttaaagatagattatagaccattag	703
Db	4	ATGACAAATNTAACTCAAAATCGCTTAAAAATATTACAAAGCCGTGCTGNNGTACCTTTAG	63
Qy	704	catatgttaacttcgactgagtgattatgaagaacttaataatgaagagatgtttctaata	763
Db	64	CGTATATCAACTTTTAATGAATATATTAAAGAACTTAACCAAGAGCGTGATTTTAAATA	123
Qy	764	aagattttaataaaggcgtccaaagattattggaagagacgtgataataagaagaagcttata	823
Db	124	AGATTTTAAATAAAGCGTTAAAGGATATTGAAACAGTCTCTGAAATATAAAGACCATATA	183
Qy	824	acaaaagagataatctcaacaacattagatgcaaatcaacaaaaaattgatgaagcta	883
Db	184	ACAAGCGAGATAACTTTACACAACAACACTTGATGCAATGAGCAAAAGTTGAAGAGGTA	243
Qy	884	aaactttacaacaagaacatggttaataagattacattcttcagctggatatttcttcatta	943
Db	244	AACGTCTTCAAGANGAACATGGTAATGAATTAACCTATCTCTNCTGTTTCTNCTTTATCA	303
Qy	944	atccggttggaagttgtttattacgcagaggtggcacatcgtaacgttatcgctacatgccc	1003
Db	304	ATCCATTGTGANGTTGTTTATTATGCTGGTGGTACATCAAAATGCATCCGGTCATCTTTCGG	363
Qy	1004	gaagtatgcaattcaatggaataataaactatgcttttagaacat	1050

DB 364 GAAGTTATGCAAGTCAATGGAATGATTATTAATGATTAATCAT 410

RESULT 9

US-09-266-417-6

Sequence 6, Application US/09266417
Patent No. 6228588

GENERAL INFORMATION:

APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-266-417-6

Query Match 20.0%; Score 256; DB 4; Length 410;
Best Local Similarity 76.2%; Pred. No. 1,1e-49;
Matches 310; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 644 atgattgtctatataatcgattataaacttaagatagattagaccattag 703

DB 4 ATGACAAATATTAACATCAATGCTTAAATATTACAAAGACCGTGTGTAACCTTTAG 63

QY 704 catgtgtgctgattgatatattgaagaacttaataatgaagaagattgtcttaata 763

DB 64 CGTATATCAACCTTAAATTAATTAATTAAGACATAAGAGGCTATATTTAAATA 123

QY 764 aagatttaataagcgctcaagaatatltgaagaagacctgataataagaagcttata 823

DB 124 AAGATTAAATTAAGCGTTAAAGATATTGAAAAACGTCCTGAAAAATAAAAAGACACTA 183

QY 824 acaaaagataatcttcaacaacaacttagatgtaactcaacaataatgtagaagta 883

DB 184 ACAAGGAGATTAACCTTACCAACCAACTGATGCAATGAGCAAAAGATTGAAGAAGSTA 243

QY 884 aaacttaacaagaacatgtaataatgaattacatttcaagctgatatcttccatca 943

DB 244 AAGCTTACAAAGNAGACATGTAATGAATTAATTAATTAATTAATTAATTAATTAATTA 303

QY 944 atccgttgaaattgtttatttaagcagtggtgacacatgtaacgttatccatgacga 1003

DB 304 ATCCATTGANGTGTATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 363

QY 1004 gaagttatgcaatgtaagaataatgtaactaactgattagaacat 1050

DB 364 GAAGTTATGCAAGTCAATGGAATGATTATTAATGATTAATCAT 410

RESULT 10

US-08-714-918-4/C

Sequence 4, Application US/08714918
Patent No. 6037123

GENERAL INFORMATION:

APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-714-918-4

us-09-509-234c-46.rni

Fri Jun 21 08:38:19 2002

FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELEPHONE: (213) 499-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-4

Query Match 17.28; Score 221.2; DB 4; Length 400;

Best Local Similarity 72.88; Pred. No. 8.2e-42;

Mismatches 0; Conservative 291; Gaps 1;

QY 205 gggccagtgattgattgataaataaagagcgttgcttcaacttttttcttaataatgaatgaatg 264

Db 400 GTCCAGTGATTGANTATGAAATCAAGNACTGCTACACTTTTCTTAAATGAAATATCC 341

QY 265 -aaatgtataaagcagcgaattgttcttcaacttcaacttcaacttcaacttcaacttca 323

Db 400 GTCCAGTGATTGANTATGAAATCAAGNACTGCTACACTTTTCTTAAATGAAATATCC 341

QY 324 atacttaataatcagcgggaaatattgtgaaatggaatggaatggaatggaatggaatggaatg 383

Db 340 AAATATGTTTAAATCAATCGTTGCTTATACCTACATACATACATACATACATACATACAT 281

QY 384 gatggaagaattagattgaacatgaagcgtttcctataaagcgtttcctataaagcgtttcctata 443

Db 280 ATACTTGAATCATGATGCGAGATTACAGGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 161

QY 444 agtaagatattcattcagtttttagatttaaaagataaaagcgttaaaagcgttaaaagcgtta 503

Db 160 AATCGGTTATCATCAGTCAGTGTAGATTAAAGATATAAAGATATAAAGATATAAAGATATA 101

QY 504 atggtatgatttaagaagaagcgttaactaagaagaagaagaagaagaagaagaagaagaagaag 563

Db 100 TATGGATGACTTAGAAAAAGAACACGGAANNAGTTNAAAGAGATGGTGTAAAGTAAG 41

QY 564 ttccctatccgaagatgaattaccctattctttagatcattt 603

Db 40 ATTTTATCTGTAAGGAGNACTACCAATTTTATGATTATTT 1

RESULT 12

US-09-265-315-4/c

; Sequence 4, Application US/09265315

; Patent No. 6187541

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

Query Match 17.28; Score 221.2; DB 3; Length 400;

Best Local Similarity 72.88; Pred. No. 8.2e-42;

Mismatches 0; Conservative 291; Gaps 1;

QY 205 gggccagtgattgattgataaataaagagcgttgcttcaacttttttcttaataatgaatgaatg 264

Db 400 GTCCAGTGATTGANTATGAAATCAAGNACTGCTACACTTTTCTTAAATGAAATATCC 341

QY 265 -aaatgtataaagcagcgaattgttcttcaacttcaacttcaacttcaacttcaacttca 323

Db 340 AAATATGTTTAAATCAATCGTTGCTTATACCTACATACATACATACATACATACATACAT 281

QY 324 atacttaataatcagcgggaaatattgtgaaatggaatggaatggaatggaatggaatggaatg 383

Db 280 ATACTTGAATCATGATGCGAGATTACAGGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 161

QY 384 gatggaagaattagattgaacatgaagcgtttcctataaagcgtttcctataaagcgtttcctata 443

Db 220 AATCGGTTATCATCAGTCAGTGTAGATTAAAGATATAAAGATATAAAGATATAAAGATATA 101

QY 444 agtaagatattcattcagtttttagatttaaaagataaaagcgttaaaagcgttaaaagcgtta 503

Db 160 AATCGGTTATCATCAGTCAGTGTAGATTAAAGATATAAAGATATAAAGATATAAAGATATA 101

QY 504 atggtatgatttaagaagaagcgttaactaagaagaagaagaagaagaagaagaagaagaagaag 563

Db 100 TATGGATGACTTAGAAAAAGAACACGGAANNAGTTNAAAGAGATGGTGTAAAGTAAG 41

QY 564 ttccctatccgaagatgaattaccctattctttagatcattt 603

Db 40 ATTTTATCTGTAAGGAGNACTACCAATTTTATGATTATTT 1

RESULT 11

US-09-265-315-4/c

; Sequence 4, Application US/09265315

; Patent No. 6187541

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/265,315

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

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Page 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 5253 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-19

Query Match 7.68; Score 97.6; DB 4; Length 5253;

Best Local Similarity 46.38; Pred. No. 1.7e-13;

Matches 396; Conservative 1; Mismatches 450; Indels 9; Gaps 2;

QY 375 ttcaataagaaggaattgaattgacataagagcttcataaagcttcacatcc 434
DB 2968 ttggcaaaattggaaagcgcttggttttaacataaagatttaagagctttatcmaa 2909
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DB 2908 agactacatccaaacacgacatgactatgattacccaattgataaataatgatgatgtt 2849
QY 495 actcaagaagaatgagtagttaagaagcgtaataactaagaagaagtaacaaaataatggtgt 554
DB 2848 attaaatagtttgaacgacgcaaatcgttcaaaaagtcgcttgcttttaaaagcaggtac 2789
QY 555 caaagtcgcttccatccgaagatgaattacattcattcattatgacattatgagaagatac 614
DB 2788 gacagtagaagcattctgattagaaagatttttaaaacatttgcctgaattatgaaatac 2729
QY 615 tacagaagaagaagatcgccgacatagaagatgatttctatataatcgaattaaata 674
DB 2728 tgggaaacgacatgcttcttaacgctgacatgatttgaatttgaatttgaattgac 2669
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DB 2668 gttgcattgaagatgacatgctgaactatttttgaattgaaagtggatccaaaagaaatatt 2609
QY 729 tgaagaacttaataagaagagatgcttcaataaagatttaataaagcgctcaagaaga 788
DB 2608 accgaagtagaattgaagattgaaattgaaattgacccgaattgcttaattgacacagaa 2549

QY 789 tatgagaagagacgtataa---taagaagcttataacaaagaagataatcttcaaca 845
DB 2548 gatataaaacattgaaagacgctataaaagcgaataatgattatgattgctgcaaaa 2489
QY 846 acaatagatgacaaatcaacaaataatgtagagctaaataactacaaagaacatgag 905
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DB 2428 tgaagattttatcttctgctgacacattatgaattgctgctgcaaaaacatatttactt 2369
QY 966 cgcaggtgacacatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgatcgat 1025
DB 2368 atatgctgctgcttcttaaaatgatttgaatttgaatttgaatttgaatttgaatttga 2309
QY 1026 atgataactatgctttagaactgaattaaacgcttataatctttagagtagtgg 1085
DB 2308 gatgattgaattgacacgctgaacatgctgaacatgctgaacatgctgaacatgctga 2249
QY 1086 ggaactgaagagacgctgaagatgtagaggaatgaatgaatgaatgaatgaatgaatga 1145
DB 2248 tgaatcgaattgaactgaacacattatgattgattgattgattgattgattgattgatt 2189
QY 1146 tgaatgattgaatgattgattgattgattgattgattgattgattgattgattgattg 1205
DB 2188 atacttgaattgaattgattgattgattgattgattgattgattgattgattgattgatt 2129
QY 1206 ctataagcacttaaa 1221
DB 2128 aattgacgaagttaa 2113

Search completed: June 20, 2002, 12:04:01
Job time: 20956 sec

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Fri Jun 21 08:38:19 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2002, 14:26:42 ; Search time 8551.36 Seconds
(without alignments)
2025.010 Million cell updates/sec

Title: US-09-509-234C-46

Perfect score: 1283
Sequence: 1 acagctaaagaattacgtga.....tatgaattacagagttaa 1283

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83.8	6.5	877	12	A2531291
2	82.2	6.4	912	12	A2551092
3	81.4	6.3	843	12	A2551618
4	81	6.3	905	12	A2550256
5	80	6.2	908	12	A2548467
6	74.6	5.8	849	12	A2546009
7	74.6	5.8	1101	12	CNS000EVL
8	74.4	5.8	879	12	CNS01RGC
9	73.2	5.7	1101	12	CNS0039G
10	73	5.7	614	12	CNS0152H
11	71	5.5	931	12	BH160272
12	70.4	5.5	1135	12	CNS033GO
13	68.6	5.3	1101	12	CNS01219
14	68.6	5.3	1101	12	CNS0153V
15	67.8	5.3	994	12	CNS04N0J
16	67.8	5.3	1007	12	CNS06X9S
17	67.6	5.3	769	12	AG134867

C 18	67.6	5.3	1201	12	CNS0167M	AL106396 Drosophila
C 19	67.4	5.3	936	12	CNS07ANM	AL143608 T7 end of
C 20	66.2	5.2	976	12	BH149983	BH149983 ENT023TRF
C 21	66	5.1	575	10	BM167050	BM167050 EST369573
C 22	65.6	5.1	768	12	CNS01AYSE	AL168683 Tetradodon
C 23	65.6	5.1	928	12	CNS00DPKY	AL071865 Drosophila
C 24	65.6	5.1	982	12	AQ225799	AQ225799 nbx0021B
C 25	65.6	5.1	1096	12	BQ9494	BQ9494 T1F7-5p6 TA
C 26	65	5.1	1059	12	CNS0022B	AL097133 Drosophila
C 27	64.8	5.1	967	12	CNS0072W	AL433362 T7 end of
C 28	64.6	5.0	867	12	CNS0054A	AL057618 Drosophila
C 29	64.6	5.0	1101	12	CNS001FB	AL060732 Drosophila
C 30	64.6	5.0	1101	12	CNS017YG	AL108658 Drosophila
C 31	64.4	5.0	981	12	CNS02BD8	AL189701 Tetradodon
C 32	64.2	5.0	1034	12	CNS0154T	AL104988 Drosophila
C 33	64	5.0	984	12	CNS03WVO	AL252575 Tetradodon
C 34	64	5.0	1036	12	CNS00599	AL057797 Drosophila
C 35	63.6	5.0	483	12	CNS02CV8	AL191645 Tetradodon
C 36	63.6	5.0	941	12	A2682404	A2682404 ENT1016TF
C 37	63.4	4.9	802	12	A2197934	A2197934 SP_1036.B
C 38	63.4	4.9	891	12	A2683582	A2683582 ENT047TR
C 39	63.4	4.9	970	12	CNS0182A	AL108796 Drosophila
C 40	63.2	4.9	660	12	BH183498	BH183498 023.L.07-
C 41	63.2	4.9	660	12	CNS07ONJ	AL620449 T3 end of
C 42	63.2	4.9	990	12	CNS0060I	AL065624 Drosophila
C 43	63.2	4.9	1101	12	CNS003BD	AL064091 Drosophila
C 44	63	4.9	1092	12	CNS020K7	AL175696 Tetradodon
C 45	63	4.9	1101	12	CNS016LI	AL106896 Drosophila

ALIGNMENTS

RESULT 1
A2531291/c 877 bp DNA linear GSS 03-NOV-2000
LOCUS ENT034TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, DNA sequence.

ACCESSION A2531291
VERSION A2531291.1 GI:11085838
KEYWORDS
SOURCE
ORGANISM
Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE
1 (bases 1 to 877)
Lofthus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)

JOURNAL
COMMENT
Contact: Brendan J Lofthus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b1ofthus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 829.
Location/Qualifiers

FEATURES
source
1. 877
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site 1: Bst I; Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

method for isolate identification. Exp. Parasitol. 77:450. The DNA was mechanically sheared to give a tight-tail distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell. Oxford University Press, 1993).

BASE COUNT	156 a	268 c	29 g	424 t
ORIGIN				
Query Match	6.5%;	Score 83.8;	DB 12;	Length 877;
Best Local Similarity	46.0%;	Pred. No. 6.9e-05;		
Matches 320;	Conservative	0; Mismatches 372;	Indels 3;	Gaps 1;
QY	217	gattatgataataaagagctgttccactttttcctaagttaattaagaataatgaataaa	276	
Db	803	GAATATGAATTAGAAAGAAGAAGATGATGATGATGAAGAAGAAGAAAGATGATGAA	744	
QY	277	aagcataaattgccttatcaaggcttgacccttatcttccttcatcaactaatcat	336	
Db	743	GATGATGATGATGAAGAAGATGATGATGACAGACAGATGATGATGAAGAAGATGATGAT	684	
QY	337	gacggtagaattattggaaatcgctgccatgatgggtttttccaataagatggaagaatta	396	
Db	683	GAAAGAGTGCATGAAGAAGATGATGAAGAAGAAGATGATGAAGATGAAGATGATGAA	624	
QY	397	ggattbgaaacaagaagccttccataaaggcttccactctctcacagtaagatatcat	456	
Db	623	GACGATGAAGCAGCGCAATATGAATTAGAAGATGATGATGAAGAAGAAGAAGATGAT	564	
QY	457	tcagttttagatttaaagaataaaaacgcgtaaagatgactcaaaaggaatggatagttta	516	
Db	563	GATGAAGATGATGAAGACGGATGAAGCACGCCAATATGAATTAGAAGATGATGATGAT	504	
QY	517	agaaagcgttaactaagaagaagtacaaaaaattggtccaaagtcogtttccatccgaa	576	
Db	503	GHAGNAGNAGTGTGATGAAGAAGAAGAAGATGATGATGAAGATGATGATGAAGAAGA	444	
QY	577	gatgaattacctattcttagatcattattggaagatactacacagaacgaaagattccgc	636	
Db	443	GATGAAGAAGATGA---TCGAAGAAGATGATGAAGATGATGATGAAGAAGAAGATGAT	387	
QY	637	gataagatgatagtttctattataatcattataaaactttaaagatagatgattagta	696	
Db	386	GATGAAGATGATGAAGACGCTGAAGACGACGACGAATATGAATTAGAAGATGATGATGA	327	
QY	697	ccattagcatatgttgacttcgatagttatattgaagaccttaataatgaaagaagattt	756	
Db	326	GAAGAAGATGATGATGAAGAAGAAGAAGATGATGATGAAGATGATGATGAAGAAGAAG	267	
QY	757	cttaataaagatttaataaagcgtcaaagatataggaaagagaccctgataataaagaa	816	
Db	266	GAAGATGATGATGAAGAAGAAGATGAAGATGATGATGNACGAACAAGATGATGATGAAG	207	
QY	817	gctttaaaaaagagataaattcttcaacaacaattagatgcaatcaacaacaaattgat	876	
Db	206	GMAGTGAGAGAGNAGNAGTGCATGAAGAAGATGATGAAGAAGAAGAAGATGATGATGA	147	
QY	877	gaagctaaaaaacttcaacaagaacatcggtaatga	911	
Db	146	GACGACGAATATGAATTAGAAGATGATGAAGAAGA	112	

RESULT 2
A2551092 DNA 912 bp linear GSS 14-NOV-2000
LOCUS ENT5F222F Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, DNA sequence.
ACCESSION A2551092
VERSION A2551092.1 GI:11176393
KEYWORDS GSS.

SOURCE	Entamoeba histolytica.
ORGANISM	Entamoeba histolytica Eukaryota; Entamoebidae; Entamoeba. 1 (bases 1 to 912)
REFERENCE	Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library Unpublished (2000)
JOURNAL	Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3343 Email: bjloftus@tigr.org
COMMENT	Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library Seq primer: M13-Forward Class: shotgun High quality sequence start: 17 High quality sequence stop: 861. Location/Qualifiers 1. 912 /organism="Entamoeba histolytica" /strain="HMI:IMSS" /db_xref="taxon:5759" /clone_lib="Entamoeba histolytica Sheared DNA" /note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In genome Sequencing: A Practical Approach, eds. M. Vaudin and B. B. Barell, Oxford University Press, 1999)."

BASE COUNT	423 a	34 c	264 g	191 t	
Query Match	6.4%	Score 82.2;	DB 12;	Length 912;	
Best Local Similarity	45.9%;	Pred. No. 0.00013;			
Matches 319;	Conservative	0;	Mismatches 373;	Indels 3;	Gaps 17;
Qy	217	gattatgataataaagagctgtttcacctttttttaagtaataagtaataatgtaataatgtaataa	276		
Db	195	GAATATGAATTAGAAAGAGAAAGAAAGATGATGATGATGATGAAGAAAGAAAGATGATGAA	254		
Qy	277	aagcataattgctttatctaagagdtggaccttatcttcccttatactaactaaatcat	336		
Db	255	GATGATGATGATGAAGAAGATGATGATGAAGAAGATGATGATGAAGAAGATGATGAAGATGATGAT	314		
Qy	337	gcagctgaaattatgtgaaactgtggccatgatgtgttttccaataagatggaagaatta	396		
Db	315	GAAGAAGATGATGAAGAAGATGATGAAGAAGAAAGATGATGAAGATGAAGATGATGAA	374		
Qy	397	ggatttgaacatgaaggtcttcaaaaggtctccctctatcttcaagtaagatacat	456		
Db	375	GACGATGAAGACGCGAATATGAATTAGAAGATGATGATGATGAAGAAGAAAGATGAT	434		
Qy	457	tcagtttttagatttaaaagataaaacgcgttaagatgtactcaaggaagtgatagttta	516		
Db	435	GATGAAGATGATGAAGACGATGAAGACGACGAAATATGAATTAGAAGATGATGATGATGAT	494		
Qy	517	agaaagcgtactactaagaaagtcacaaaaaaatggtgtcaaaagtcctgtttcctatccgaa	576		
Db	495	GNAGAACAGATGATGATGAAGAAGAAAGATGATGATGAAGATGATGATGAAGAAGAA	554		
Qy	577	gatgaattaccttatcttttagatcatattatggaagatactacagaacaaagagttcgcc	636		


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Db      76 GATGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 135
      376 ttcaataagatggaagaattgaattgaacatgaaggttcataaaggtccatccat 435
      136 GATGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 195
      436 atcttaagaatgaatcatcattcagtttagttaaagaataaagcgttaagaatgta 495
      196 GATGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 255
      496 ctcaagaagaatgatagtttaagaagcgtatatacttaagaagttcaaaaatggtc 555
      256 TTGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 315
      556 aaagtcggttcctccatccgaagaatgaattacattcatttagatcattatggaagat 615
      316 GAAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 372
      616 acagaagaagaagatgcgcgaatagagaatgattcattataatcgttaataatc 675
      373 GATGAGAGAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 432
      676 cttaagaatgaatcattagatcattatgattgactcgatgagatgataatgaaga 735
      433 TTGAGAGATGATGATGAGAGAGATGATGAGAGAGATGAGAGAGATGAGAGAGAT 492
      736 cttaagaatgaagaatgattcattataaagaatgaagtcgtcaagaatgag 795
      493 GATGATGATGATGAGAGAGATGATGAGAGAGATGATGAGAGAGATGAGAGAGAT 552
      796 aagagaacctgataaagaagctatacaagaagaatccttaacaacaatagat 855
      553 GAAGAGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 612
      856 gcaaatcaacaataatgattgaagctaaacttaacaagaagaatgataatga 911
      613 GAAGAGAGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 668

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RESULT 6
LOCUS   A2546009/c 849 bp DNA linear GSS 14-NOV-2000
DEFINITION
ENTPWS37F Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION
VERSION A2546009
KEYWORDS
SOURCE  A2546009.1 GI:1167130
ORGANISM
Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE
1 (bases 1 to 849)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3343
JOURNAL
COMMENT
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 26
High quality sequence stop: 796.
Location/Qualifiers
1..849
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"

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/clone_1lb="Entamoeba histolytica Sheared DNA"
/Note="Vector: pROSL; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broch cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaundin and B.
Barrell, Oxford University Press, 1999)."
BASE COUNT 199 a 236 c 43 g 371 t
ORIGIN

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Query Match 5.8%; Score 74.6; DB 12; Length 849;
Best Local Similarity 44.9%; Pred. No. 0.0025;
Matches 284; Conservative 0; Mismatches 349; Indels 0; Gaps 0;

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      388 gaagaatgagattgaacatgaaggttcataaaggtccatccattacaagta 447
      730 GAAATGTGAAATGGAACATGATACCGATTGAGAGACATGAAATTGGAAGAGATGAT 671
      448 agatcattcagtttagatttaaagaataaagcgttaaagatgactcaagaagatg 507
      670 GATGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 611
      508 gatagtttaagaagaagcgtataactaagaagtcataaagaatggtgataagtcgttc 567
      610 GAAGAAGAAGATGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 551
      568 ctatccgaagatgattaccattcatttagatcatttagaagatactacaagaagaa 627
      550 GAAGATGAGAGAGATGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 491
      628 gaattccgcgaatagatgattcattataatcattcatttaaaacttaagaataga 687
      490 GAAGATGAGAGAGATGATGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 431
      688 gattagatacattagatcattgactcgtatgataattgaagaacttaaatga 747
      430 GATTTGAAAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 371
      748 agagaatgattcattataagaatttaagaagcgtcaagaatattgaagaagacgtat 807
      370 GATGAGAGATGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGATGAGAT 311
      808 aataagaagaacttaacaagaataaacttcaacaacaatagatgataatcaaca 867
      310 GATGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGATGAGATGAGATGAGAT 251
      868 aaattgataagcctaaacttaacaagaagaatgataatgaattacattcagct 927
      250 GATGAGAGATGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGATGAGAT 191
      928 ggtatttcttattatcgcgttggaagtgttttctcgaagttggaagcagatcagat 987
      190 GAAGATGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAT 131
      988 tatcgtactatgcgcgaagatgataatca 1020
      130 GATGATGAGAGATGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAT 98

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RESULT 7
LOCUS   CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
DEFINITION
Drosophila melanogaster genome survey sequence 77 end of BMC:
BACR29B23 of RP11-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

```

Dd	864	WAATWATAAANAATAAWATTWTWTWTWWAAWATAAANAAAAA 923 : : :
Qy	869	aattgataagctaaaaacttacaagaacatggtaagtacctatttcagctg 928 :: : : : : : : :
Db	924	AAGAAAATAAAMWTTATATTTATTAAATWTATGWATWTATTAATGTTW 983 : : : :
Qy	929	gatattttcattaat 945 : : :
Db	984	TATWTATATATWTATT 1000 : : :
<hr/>		
RESULT	8	
CNS01JRG/c		
LOCUS	CNS01JRG	789 bp. DNA linear GSS 12-JUN-2001
DEFINITION	Anopheles gambiae GSS T7 end of clone tAD07 of NotreDamel library from strain PEST of Anopheles gambiae genomic survey sequence.	(Anopheles malaria mosquito),
ACCESSION	AL147405	
VERSION	ALI147405.1 GI:7005551	
KEYWORDS	GSS;	
SOURCE	African malaria mosquito.	
ORGANISM	Anopheles gambiae	
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.		
REFERENCE	1 (bases 1 to 879)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr) - Web : www.genoscope.cns.fr)	
REFERENCE	2 (bases 1 to 879)	
AUTHORS	Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France	
COMMENT	This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.	
<hr/>		
FEATURES	Location/Qualifiers	
source	1.. 879	
/organism="Anopheles gambiae"		
/strain="PEST"		
/db_xref="taxon:7165"		
/clone="tAD07"		
/clone_lib="NotreDamel"		
/note="end : T7"		
BASE COUNT	66 a 38 c 1 g 670 t 104 others	
ORIGIN		
<hr/>		
Query Match	5.8%; Score 74.4; DB 12; Length 879;	
Best Local Similarity	39.7%; Pred. No. 0.0027;	
Matches 234; Conservative	54; Mismatches 299; Indels 2; Gaps 1	
QY	324	atacttaaatcatgcgcgtgaatttgaaatgctgccatgatcggttttcataaa 383 : : :
DB	879	AWATGTAAATATTATAAAAAAAAAATATATAAAAAAAAAAAAAAAAAAAAAAG 820 : : :
QY	384	gatggagaattaggattgcaacatgaagctttcataaaggctccatctactaca 443 : : :
DB	819	TAGTAATATATTGGATWGATGTATAAAAAAAAAAAAAAAAAAAAAAGTAAATA 760 : : :
QY	444	agtagaatcattcagtttgttatgatttaaagataaacggctaagatgactcaa 503 : : :
DB	759	AAAAAARAATATCTGAANKAWAAAAAATATAGTAGAAAAARATAGWGAWADKKAKK 700 : : :
QY	504	aatggatagtttaagaagcgttaatcactaagaagtacaaaatatgggtccaagtccg 563 : : :
DB	699	GKTRAEKGWAAAIAAAAAAAAAAANTATATAAAAAAGKATATAAAAAAAAAAWAAAA 640 : : :

[illegible]

OY 564 ttccatccgaagatgaattacccttagatcatttctgaagatactcagaac 623
 DB 639 AAAAGTTTATKAKMKAMGAAAAAKGAAAAATTGWWGTTDAAAAAATAGCAAAAA 580
 OY 624 gaaagatcgccgataagatagatctcattatcatatcatgaataacttaaga 683
 DB 579 AAGAGAGWAGKRGARAAAAAAGKAAAAAATGTTARAAAATGAAAAA 520
 OY 684 tagagatttagtaccatagatatgttagcttgatagatatactgaactataa 743
 DB 519 KAKATRRRAAAAAAAMKRGAAKR--GAGAAAAARAGATWAKKAAAAA 462
 OY 744 tgaagagatgtcttaataagaattaaagcgctcaagaatattgaagagacc 803
 DB 461 TDAATAAAATKAWTTBAAAAAGAKAGKATATCTDRAAAAAAATAAANA 402
 OY 804 tgataataagaagctatacaaaagagatacttcacacacattgataatca 863
 DB 401 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 342
 OY 864 acaaaatttgatgaagctaaacttaacacagaacatgtaataga 912
 DB 341 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 293

 RESULT 9
 CINS00396/c 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
 DEFINITION BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 A1063921
 VERSION A1063921.1 GI:4941778
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 REFERENCE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org/The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mamoser in Peter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

 FEATURES
 source 1. 1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR08K10"
 /note="end : TET3"
 BASE COUNT 201 a 64 c 131 g 202 t 503 others
 ORIGIN
 Query Match 5.7%; Score 73.2; DB 12; Length 1101;
 Best Local Similarity 17.6%; Pred. No. 0.0042;

Matches 119; Conservative 285; Mismatches 270; Indels 2; Gaps 1;
 OY 276 aaagcataattctcttcttaagagttgacccattctctcattcaataactaaca 335
 DB 1091 WDRDTRKDDMDWTWKMTWKKRADRRWAGDDADRWAMWDGAGTWTWTWMMWMAATWD 1032
 OY 336 tgaagtgaaattatgaatgagtcggtcgaattgattgatttcaataagaatgaatt 395
 DB 1031 TWMKMMWMAATATKTDTWTWTRAMPADWAGDRGACKRRDAAATDADGAGDRGGRK- 971
 OY 396 aggaattgacataagagcttcataaagctccatccatcttctacaaagataatca 455
 DB 972 -RKDKDRKDGDDDKGKKKAKAKATKWDMDMDKDKWMDKADKDRKADDDGAG 914
 OY 456 ttcagtttagatttaaaagataaagcgttaagatgactcacaagaaatgataatt 515
 DB 913 DKDDGKXADDDYDGTKDDDDKMDWDKAKGTWSDATWMAATDMMWMAADMM 854
 OY 516 aagaagcgttaacttaagaagaatgacaaaatggtgcacagtcgcttcatacga 575
 DB 853 TWDAADDMWADDRWDAMWAKMDAMWAKRTADRRDMDRAGRGARRRRKRAADK 794
 OY 576 agatgaattaccatctttagatcattatgaagaatactacagaacgaagatgcg 635
 DB 793 RDAADDDDAATTTTWTTRDTRDMDKMTDTWTWMAADRTWDRDDDDBRAGTAGRK 734
 OY 636 cgatagagatgatttctattataatcgattaaatacttcaagatgattatgt 695
 DB 733 WRRTWKRRMRRTDRWDADDDYADRRRRRGGDDADGKKTKGRRRRRRRAWDR 674
 OY 696 accattgcatagttgactcgatgagatatttgaaagacttaataagaagaatgt 755
 DB 673 DAWWADAAMWTTDTDTDDMDKRRRRGARRRRRTTARAAWMTWAMDMKMKR 614
 OY 756 tottaataaagatttaagaagcgctcaagaatattgaagaagacctgataaaga 815
 DB 613 ADRWRWMAADTWDARKADRKARARARADAAABADRTTKKTATATWTMAA 554
 OY 816 agctatacaaaagataatcttcaacaacattagatgacaaatcaacaaaatga 875
 DB 553 RAAMWAMWMAATTTATWTTTWTWTTTWTWTTTAAWMAWMAWTTWMAWMAA 494
 OY 876 tgaagctaaacttcaacaagaacatgtaagattacttactttagtgcgtatatt 935
 DB 493 WAAAAAAMWATTTTWTWTTTWTWMAAAMWMTWTTTWTWMAATTTTWTWT 434
 OY 936 ctcttcaatccgtt 951
 DB 433 TWMAATTTATTTTWT 418

 RESULT 10
 CINS0152H 614 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence S96 end of BAC
 DEFINITION BACN12N03 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 A1104915
 VERSION A1104915.1 GI:5616929
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 614)
 REFERENCE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -

RESULT	12	1135 bp	DNA	linear	GS5 15-MAY-2000
CNS0333Q					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
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[illegible]

b 9 ANAAAAANAAA 68

y 501 aggaatgtagtatttaagaagcgtatactactaagaagtcacaaaaaatgggtceaaagt 560
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 b 69 AAA 128
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 y 561 cggttctatccgaagatgaattacctctttagctcatttagtggaagatactacaga 620
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 b 129 AAA 188
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 y 621 aacgaagaagctgcgcgatgagatgattgttcttataatcgattaacaatactttaa 680
 || | | | | | : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
 b 189 AAAAAAAAAAAAAAAAAAAAAAAAAAWAAAAAWATATAAAAAAAAAAAAAAAAAAAAAWAAA 248
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 y 681 agatagagtattagaccattgcatgttgcttcctgcatgatttggaagaacttaa 740
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 b 249 AAAWAATWAAAA 308
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 y 741 taatgaagaagatgttctaataaagatttaataagcgcgctcaagatatgtgagaag 800
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 b 309 AATAWAAAAAIAAAAA 368
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 y 801 acctgataagaagcttatacaaaaagagataatcttcacacacaaattagatgc aa 860
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 b 369 AATAAAWAAAAAIAAAA 428
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 y 861 tcacaaaaaattgatgaagcttaaacaaactcacacaagaacatggtaatgaa 912
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 b 429 AAAAAAAAAAAAAAAAAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAWAAAAIA 480
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 15
CNS04NOJ      CNS04NOJ      linear   GSS 21-MAY-2000
LOCUS        Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION   Tetraodon nigroviridis genome survey sequence
ACCESSION    AL298972.1 GI:8037822
VERSION      GSS; genome survey sequence.
KEYWORDS     Tetraodon nigroviridis.
SOURCE       Tetraodon nigroviridis.
ORGANISM     Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neteleostei;
              Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
              Tetraodontidae;
REFERENCE     1 (bases 1 to 994)
AUTHORS      Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
              Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
              Weissenbach,J.
TITLE        Characterization and repeat analysis of the compact genome of the
              freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 994)
AUTHORS      Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
              Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
              Saurin,W. and Weissenbach,J.
TITLE        Human gene number estimate provided by genome wide analysis using
              Tetraodon nigroviridis DNA sequence
JOURNAL      Unpublished
REFERENCE     3 (bases 1 to 994)
AUTHORS      Genoscope.
TITLE        Direct Submission
COMMENT      Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases
              This sequence is a single read and was generated as part of a large
              scale clone-end sequencing project of the Tetraodon nigroviridis
              genome. For more information, please take a look at
              http://www.genoscope.cns.fr/Tetraodon.
              Location/Qualifiers
                  . 1..994
                   /organism="Tetraodon nigroviridis"
                   /db_xref="taxon:99883"
                   /clone="122P04"
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/clone_11b-"G"
/note="Genoscope sequence ID : COBG122DH02LPI-end : T7"
BASE COUNT 543 a 49 c 36 g 194 t 172 others
ORIGIN

Query Match 5.3%; Score 67.8; DB 12; Length 994;
Best Local Similarity 38.0%; Pred. No. 0.035;
Matches 304; Conservative 52; Mismatches 440; Indels 4; Gaps 2;

```

QY 471 aaaaataaaacgctaaagtctaaccaagaagatgatagtttaagaagcgttaac 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 ATAKGAKAAACCKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 238

QY 531 taagaagtaacaaaaaagtgtctaaagcttcctacccaagaatgaattactat 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 KCCACACAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 297

QY 591 ctttagatcattatgaaagatactacagaacgaagagttccgcatagagatgag 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 NNNNNNANNAVNNNSAAVNNVTBGAAGAAAAAATNANNAANAAAAAATNANNA 357

QY 651 ttctataatcgaatgaataactttaagaatagatagtagccattagcattagt 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 AAAAAAAMAAAAATNANNAANAAAAAATNANNAANAAAAAATNANNAANAAAA 417

QY 711 tgactcgatgctatattgaagaacttaataatgaagaagagttcttaataagatt 770
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Db 418 AATATTTATATATATATATATATATATATATATATATATATATATATATAT 477

QY 771 aaataagcgcccaagatatttggaagagaccgtgataataagaagcttatacaaaag 830
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QY 951 tgaagttgattatgaagcggtgcacacgaatcgctacgacatgacgaagctta 1010
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Db 951 tgaagttgattatgaagcggtgcacacgaatcgctacgacatgacgaagctta 1010

QY 1011 tgcattcaatggaataatgataactatgcttgaagaacatggaatgaacgttataatt 1070
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Db 775 AAAAAAATATATATATATATATATATATATATATATATATATATATATAT 834

QY 1131 aaaaagcctataatgctgaatgataatgataatgataatgataatgataatgata 1190
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Db 835 AAAAAATATATATATATATATATATATATATATATATATATATATATAT 894

QY 1191 accatgtaacatctataacgacactaaagaagtaagaagaatagatttttaccac 1250
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Db 895 ATAAAAAAMTATATATATATATATATATATATATATATATATATATATAT 954

QY 1251 ccaattatcattatgaaa 1270
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Db 955 TTAATTTTATATATGAAA 974

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GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: June 20, 2002, 12:03:10 ; Search time 12428.6 Seconds
(without alignments)

Title: US-09-509-234C-1
 Report number: 1338

Sequence:

I nnnnnnnnnnnnnaatga.....gaaattcacagagttaann 1328

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl :*

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10:  gb_ro.*
11:  gb_sfr.*
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14:  gb_vl.*
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16:  em_fun.*
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29:  em_vl.*
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33:  em_hlg_inv.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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44	755	56.9	1328	6	A971445	Sequence 1
45	754	56.8	1371	6	A971497	Sequence 53
1	739.4	55.7	1305	1	SAFEHMA	X17688
2	738	55.6	1305	6	A97186	Sequence 10
3	738.2	55.6	1306	1	A97183	Sequence 10
4	736.2	55.4	1306	1	A97183	Sequence 10
5	736	55.4	1306	1	A97183	Sequence 10
6	736	55.4	1306	1	A97183	Sequence 10
7	736	55.4	1306	1	A97183	Sequence 10
8	733	55.2	1343	6	A97186	Sequence 52
9	733	55.2	1343	6	A97186	Sequence 52
10	731	55.0	1263	1	A9709667	Staphylococcus aureus
11	730.4	55.0	4434	1	A9709667	Staphylococcus aureus
12	730.4	55.0	4434	6	A9715015	Sequence 1
13	729.4	54.9	1557	6	A9715015	Sequence 1
14	729.4	54.9	1557	6	A9715015	Sequence 1
15	727.2	54.8	1877	7	SEU03713	Staphylococcus aureus
16	724.6	54.6	1563	1	A9714661	Staphylococcus aureus
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18	694.2	52.3	1263	1	A9715332	Staphylococcus aureus
19	694.2	52.3	1263	1	A9715332	Staphylococcus aureus
20	691.2	52.0	1254	1	A9709664	Staphylococcus aureus
21	690.2	52.0	1195	6	A97186	Sequence 52
22	689.4	51.9	1583	6	A97190	Sequence 46
23	689.4	51.9	1583	6	A97190	Sequence 46
24	679.4	51.2	1257	1	A9714663	Staphylococcus aureus
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26	676.2	50.9	1260	1	A9715333	Staphylococcus aureus
27	676.2	50.9	1260	1	A9715333	Staphylococcus aureus
28	676.2	50.9	1260	1	A9715333	Staphylococcus aureus
29	676.2	50.9	1260	1	A9715333	Staphylococcus aureus
30	676.2	50.9	1260	1	A9715333	Staphylococcus aureus
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32	676.2	50.9	1260	1	A9715333	Staphylococcus aureus
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ALIGNMENTS

	RESULT	1	A97445.	1328 bp.	DNA	linear	PAT 26 -JAN-2000
BASE COUNT	DEFINITION		Sequence 1 from Patent M0916780.				
ORIGIN	ACCESSION		A97445				
	KEYWORDS		A97445.1 GI:6780791				
	ORGANISM		Staphylococcus sp.				
	REFERENCE		Staphylococcus sp.: Bacillus/Clostridium group: Bacillus/Staphylococcus group; Staphylococcus. I (bases 1 to 1328)				
	AUTHORS		Gale,J., and Vanoutfel,P.				
TITLE	GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS		Patent: NO 9916780-A, 1 08 APR 1999;				
JOURNAL	GATA JENM 1999;17(1):14-15		(US)				
FEATURES	source		location/Qualifiers				
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Oy	CGGGTTAAATAGCCCATGTACCAATTATTCAGCAGTATTAATAAATAATGAAGATAAAAAG	1324
Bz	AATTAACAATTAAATAGAACGCACACTAGCTAGCAATAGAAATTTACAGTGCTTA	1371

RESULT

LOCUS	SAFEA	3446 bp	DNA	linear	ECT 19-JUL-1995
DEFINITION	S. aureus factor essential for expression of methicillin resistance (fema) gene, complete cds, and trpA gene, 3' end.				
ACCESSION	X17668	M23918			

KEYWORDS
SOURCE

ORGANISM	Staphylococcus aureus
Bacteria: Firmicutes: Bacillus/Clostridium group	Bacillus/Staphylococcus group: Staphylococcus.

AUTHOR'S JOURNAL

REFERENCE 2 (bases 1 to 3445)
AUTHORS Berger-Bachli B., Barberis-Maino L., Strassle A. and Kayser F. H.
TITLE Fema, a host-mediated factor essential for melicillin resistance

JOURNAL
MEDLINE

FEATURES	COMMENT
Location/Qualifiers	draft entry and computer-readable sequence for (1) kindly provided by B. Berger-Baechli, 11-APR-1989.

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CDS

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Best Local similarity 56.9%; Pred. No. 8.7e-109;
Matches 741; Conservative 0; Mismatches 562; Indels 0; Gaps 0;

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OY 74 aaagatatttaccgcnagaagatltngnmthtactanagannatgcn 133
DB 61 TATATCATTTACCAATTCAGATTCAGATTAATACATACATACCA 120
OY 134 nccenatgtagtngatnaaanaanaanaanaanaanaanaanaanaanaana 193
DB 121 ATCACTTACTGTTATATATATATATATATATATATATATATATATATAT 180
OY 194 gcnlucgcnatgaatnaatlttactnaatlttactnaatlttactnaatlt 253
DB 181 GCAATGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 240
OY 224 tctnaanaanaanaanaanaanaanaanaanaanaanaanaanaanaana 313
DB 241 TATGATATATAGAGATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 300
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OY 374 gggagatnnnnnnaatgcnagaagatltngnmthtactanagannatgcn 433
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OY 494 gntnnatlttannnnnaanaanaanaanaanaanaanaanaanaanaana 553
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OY 514 gannlncnatttngatcatttactnaatlttactnaatlttactnaatlt 673
DB 601 GAACTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 560
OY 574 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 733
DB 661 AGGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 720
OY 734 ntngcnatlttannnnngntnnnnngntnnnnngntnnnnngntnnnn 793
DB 721 CTATGCTTATATATATATATATATATATATATATATATATATATATAT 780
OY 794 antaagaannnnnaanaanaanaanaanaanaanaanaanaanaanaana 853
DB 781 AATTAAGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 840
OY 854 nnnnaanaanaanaanaanaanaanaanaanaanaanaanaanaanaana 913
DB 841 TTTATATATATATATATATATATATATATATATATATATATATATAT 900
OY 914 gnnannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 973
DB 901 GCTTAAATATATATATATATATATATATATATATATATATATATATAT 960
OY 974 ataaatcctnnnngntnnnnngntnnnnngntnnnnngntnnnnngnt 1033
DB 961 ATTAATTCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 1020
OY 1034 gcnngnntatgcnatlttactnaatlttactnaatlttactnaatlt 1093

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DB 1021 GCAGCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1080
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OY 1154 tnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1213
DB 1143 ATTAATTCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 1200
OY 1214 cctnnnaanaanaanaanaanaanaanaanaanaanaanaanaanaana 1273
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LOCUS Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
DEFINITION genome, section 5/10.
ACCESSION AP003133 B0000018
VERSION AP003133.2 GI:14349175
SOURCE Staphylococcus aureus subsp. aureus N315 (sub-species:aureus N315, strain:N315) DNA.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (sites)
AUTHORS Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,T., Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Kuwano,H., Hosoyama,A., Sekimizu,K., Hirakawa,H., Kubara,S., Goto,S., Yabuzaki,J., Sekimizu,K., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
TITLE Whole genome sequencing of methicillin-resistant Staphylococcus aureus 357 (9264), 1225-1240 (2001)
JOURNAL Lancet 357 (9264), 1225-1240 (2001)
MEDLINE 21311952
REMARKS 1 to 303750
AUTHORS Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuwano,H., Hiramatsu,K.
TITLE Direct Submission
JOURNAL Submitted (30-JAN-2001) Kenichi Aoki, National Institute of Technology and Evaluation, Biotechnology Center, ZChome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
COMMENT (E-mail:aoki.kenichi2@meti.go.jp, URL:http://www.bio.nite.go.jp/ Tel:81-3-3461-1972; Fax:81-3-3461-8624)
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Query Match	Similarity	55.2%	Score	7.3	DB	1:	Length	1343:
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Db	61	aaatgaagatttccaaatttcaacgacmaagaenlttmgmmtttacacgmmatgacgn	73					
OY	74	aaagaaatcttccacaaann	133					
Db	121	aaagaaatcttccacaaann	133					
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[illegible]

[illegible]

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					1263 bp DNA linear BCT-02-KOV-1998
					GI:38206623
					Staphylococcus haemolyticus. Bacteria: Firmicutes: Bacillus/Clostridium group: Bacillus/Staphylococcus group: Staphylococcus. 1 (bases 1 to 1263) Vanunifel, P., Heusterpreute, M., Bouyer, M., Philippe, M. and Gail Vanunifel, P. Characterization of femA from Staphylococcus hominis, Staphylococcus saprophyticus and Staphylococcus haemolyticus and femA-based discrimination of staphylococcal species Res. Microbiol. (1998) In press 2 (bases 1 to 1263) Vanunifel, P., Heusterpreute, M. and Gail, J.-L. Direct Subtyping (1998) LCM, UCL, Clos Chapelie-aux Champs Bruxelles 1200, Belgium 30/3046, location/Qualifiers
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	Oy	77	aggacttatccgcgaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn	136	
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	Oy	137	cannatagtcnagaataanaanaanaanaaangangnatctgcncgtlgnltmtnaengcn	196	


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Db 3164 TATATGTTTATTTAAGAGTTCACCTACCTCCATATATTTAAATATGAG 3223
Oy 374 gggagagatlnnngnaaaegcngngnangaltggnltngatlnaantlnnnnnnn 433
Db 3234 GCGAATAATAGTGAATACAGTCATGATGATTTGATGATATGATGAGGTTTGA 3283
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Db 3284 TATTAACACAGAGATTCACAAAGGATTTGCTGATATGCAATTCATATCATCT 3343
Oy 494 gntlnaantlnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 553
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Oy 554 aagngagagatlnnngnangaltggnltngatlnaantlnnnnnnnnnnnnnnn 513
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Db 4064 CCAATTAATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGAT 1325
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Db 4117 ---ATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGAT 1443

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VERSION AM145015.1 GI:14283580
SEQUENCE synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 4434)
AUTHORS Kimmerly, W.J.
TITLE Stephylococcus epidermidis nucleic acids and proteins
JOURNAL Patent 4,434,373 17-MAY-2001;
PATENT GROUP LIMITED (GB)
FEATURES
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        /note="synthetic nucleic acid sequence"
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Best Local Similarity 57.3%; Pred. No. 1.2e-107;
Matches 752; Conservative 0; Mismatches 549; Indels 11; Gaps 1;
Oy 14 aaaaagaatlnnngatlnnngatlnnngatlnnngatlnnngatlnnngatlnnngat 73
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Db 3104 TATTAATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 3163
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Db 3344 GTTCTAAATTTACCAACCAAGGATTTGATGATGATTTGATGATGATTTGAT 3463
Oy 514 gntlnaantlnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 573
Db 3404 AACGTTAATCTTAAAGATTTAAGGATTTGATGATGATTTGATGATGATTTGAT 3463
Oy 574 gntlnaantlnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 573
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Oy 574 gngagagatlnnngnangaltggnltngatlnaantlnnnnnnnnnnnnnnnnn 733
Db 3524 AGAGAGATTTGATTTATTCACACATTTACCAACATTTAAGGATTTGATGAT 3583
Oy 734 ntngatlnaantlnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 793

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RESULT 12
 LOCUS AM145015
 DEFINITION Sequence 3737 from Patent WO0134809.
 ACCESSION AM145015
 4434 bp DNA linear PAT 31-MAY-2001

RESULT 15
 LOCUS SED23713 1877 bp DNA linear BCT 04-FEB-1997
 DEFINITION Staphylococcus epidermidis factor essential for methicillin
 resistance fema (fema) gene, complete cds.
 ACCESSION U03713
 VERSION 03713.1 GI:1815617
 KEYWORDS Staphylococcus epidermidis.
 SOURCE Staphylococcus epidermidis.
 ORGANISM Staphylococcus epidermidis.
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Bacillus/Staphylococcus group; Staphylococcus.
 REFERENCE 1 (bases 1 to 1877)
 Albom, W.E., Jr., Hoskins, J., Thal, S., Flokovitch, J.E., Hayes, C.A.,
 et al. 1997. Isolation and characterization of fema and femB from Staphylococcus
 epidermidis.
 JOURNAL Gene 180 (1-2), 177-181 (1996)
 MEDLINE 97128824
 REFERENCE 2 (bases 1 to 1877)
 Albom, W.E., Jr.
 AUTHORS Direct Substitution
 TITLE (29-Mar-1995) William F. Albom, Jr., Lilly Corporate
 JOURNAL Center, 1111 North Company, Indianapolis, IN 46285-0425, USA
 FEATURES
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 RYSLMLANKSANDVLMKDGKLRNKKVKKYKGLFSELELIFSEPDVSE
 TKDFADRESFYENFKRKYGLVPLAYINFDYIELNEENLNDNMALQIE
 KREPKFAHKKREMLDQIDNQKINEANIKCEHNEPLISAEFTINPEVETIA
 GQTSNRHRAAGSYVQRMKINIALEGRINRITGISTSDAEDMGVATFAGID
 ADVISYGDITAPKINRINIAKLNK"
 BASE COUNT 727 a 225 c 337 g 588 t
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 Best Local Similarity 57.2%; Pred. No. 4.4e-107;
 Matches 750; Conservative 0; Mismatches 551; Indels 11; Gaps 1;

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 Db 579 TATATATGTTATATTAAGAGTTGCCATACCTTCATATCATATTTAAATCA 738
 Oy 374 gngnannltnnngnaaagcngnnaagatlggnlntnngltnnntnntnntn 433
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 Oy 434 Ltnnaaanaagntltnnntnntnntnntnntnntnntnntnntnntnntn 493
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 Oy 918 nannnaaagcnaaanaaagcngnnaaagcngnnaaagcngnnaaagcngn 613
 Db 919 AAGCTATATCTTAAAGATTTAGCAAAATGAGTCCCTTTATCTGCAAGAA 978
 Oy 978 gannlncnaltlntngntcattnagatnagatnagatnagatnagatnagat 673
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 Oy 854 nnnnaaann 913
 Db 1219 CATACAAAGAAATTTAGCAACACCTGATACCAATACCAACAAATATATAG 1278
 Oy 914 gnnann 973
 Db 1279 GCTAAAGATTTAAAGCAAGATGCAATGATATACCATCTCTGCTCTTTATA 1338
 Oy 974 alnaatcctntgaagntnntnntnntnntnntnntnntnntnntnntnnt 1033
 Db 1339 ATTAATCTGTTGAGTGTATACACCTGATGAGATTTGATATGATATTT 1398
 Oy 1034 gcnngnagnttgcmtncatagcnnntgntaantlgaatnntnntnntnnt 1093
 Db 1399 GCGAGAGATTTGCGTTCAATGATGAGATATACATGATATGATATGATAT 1458
 Oy 1094 nnnnaaagcngnnaaagcngnnaaagcngnnaaagcngnnaaagcngn 1153
 Db 1459 CGGTATATATTTGATATGATGATGATGATGATGATGATGATGATGAT 1518
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 Oy 1274 nnnltnnn 1325
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Search completed: June 20, 2002, 22:09:12
Job time: 36362 sec

PF 28-SEP-1998; 98NW-BE00141.
PR 26-SEP-1997; 97EP-N074145.
PR (BPRN-1) BELGIAN MIN NAT DEFENCE.
PA (DTLO-) ONIV CATHOLOIE LOUVAIN.
PI Gata J, Vannuffel P;
PI WPI; 1999-28/521/74.
DR P-PSDB; MA108211.
New *Staphylococcus*-specific oligonucleotides
PS Claim 27: fig 12: 48bp; English.
XX This invention describes novel *Staphylococcus*-specific oligonucleotides
CC based on the consensus *Staphylococcus* sequences which are used to
CC detect and/or identify *Staphylococcus* species for detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC application, the identification and/or quantification of various *Staphylococcus*
CC sequences which are specific to known or unknown *Staphylococcus* species.
CC Since the *femA* sequence is similar to the *femB* sequence, the
CC oligonucleotides can also be used for the molecular genotyping of *femA*
CC genes of different *Staphylococcus* species or the phenotypic characteriza-
CC tion of *Staphylococcus* strains. The oligonucleotides can be used for
CC the *femA* nucleic acid tests to identify inhibitors, e.g. antibodies or
CC anti-sense oligonucleotides, for blocking expression of the *femA*
CC nucleic acid sequences. They can also be used for producing vaccines
CC against *Staphylococcus* infections.
XX
XX Sequence 1342 BP: 544 A: 161 C: 217 G: 420 T: 0 other:
SO
Query Match 54.4%; Score 723; DB 20; Length 1342;
Best Local Similarity 57.94; Prod. No. 3-56-139;
Matches 733; Conservative 0; Mismatches 531; Indels 1; Gaps 1

[illegible]

OS Staphylococcus epidermidis.
 XX MO200134809-A2.
 PD 17-MAY-2001.
 XX 09-NOV-2000; 2000MO-US30782.
 PF 09-NOV-1999; 9905-0164258.
 XX (GLAXO) GLAXO GROUP LTD.
 PA KIMEXEY MO;
 PI WPI: 2001-216495/33.
 DR P-PS08; A0681350.
 PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 useful for vaccinating against infections, e.g. endocarditis -
 XX
 PS Claim 8: Page 95: 2189pp: English.
 XX A0681304 to A0681370 represent nucleic acids (i) encoding polypeptides
 CC (11), given in A0681454 to A0681520, from Staphylococcus epidermidis
 CC (11) and (12) and the nucleic acids (1) may be used to produce the
 CC 5' epidermidis polypeptides (12) via the production of vectors the
 CC containing them which are used to produce host cells which express the
 CC polypeptides. The polypeptides (12) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for
 CC treatment of S. epidermidis infections, e.g. epidermidis genomic DNA
 CC A0681304 represent species from the present invention. A0681371 to
 CC A0681370 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequence given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472.
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX Sequence 1179 BP; 456 A; 144 C; 212 G; 367 T; 0 other:
 50
 Query Match 51.2% Score 680; DB 22; Length 1179;
 Best Local Similarity 58.0%; Pred. No. 1.4e-130;
 Matches 680; Conservative 0; Mismatches 492; Indels 0; Gaps 0;

OY 452 nmanngnltgancnmmmmcaatlmngnlnmncnltgntlnatltanmmn 511
 DB 361 ccaaaagatltgactccgtcattcaaacccggtatgttccgtccaaatlttgcaaac 420
 OY 512 aaaaamcmanganmtlnmnaamnatlgatgntmngnaamngnaaanaaa 571
 DB 421 aaagtgcatagtatgtttaaanaaacgtggtttaaagaacgtlaaataaanaa 480
 OY 572 gtnanaanaagtgngnaaagtmnmtlnmnaaagaangnmtlnmncn 631
 DB 481 gtaagaanaagtgatlaaagtcgttcaaccgaagaagtlacacatcttg 540
 OY 632 tcatataganaatcacnmgncnngnncnngnmtlnmngatngnngnmtntan 691
 DB 541 tcatltgagaagatcacctcgaaactaaagatlttgcatagagaagatgtttat 600
 OY 692 tanangnmtlnmnaatlnaagaangnmtlnmngnltgntatatanatt 751
 DB 601 tacaacgttcaaacattataaagacgtgttctgtaccacgtccatcaatctc 660
 OY 752 gtagntmtlnmngatlnmngnngnngnngnmmmtlnanlaaagennnaanaa 811
 DB 651 gtaggtatagaggaactaaatlaagaaagatgtgttaataaagatlatataa 720
 OY 812 gcmtnaangnanaangnncngnngnnaaanaaanaangcmmnaaanaamman 871
 DB 721 gcttlaaagaacatlgagaagagtcgaatlaaagaacatacaabaagaat 780
 OY 872 ntnaanaancnmtmngcnaanaagcaanlnmngnngnmmmtlnmnaam 931
 DB 781 ttagaacacacactgtatgcacatcgcaaaaatlaatgaagcataaactaaacaa 840
 OY 932 nancatgnaagaattacacatnctngcngnctnctlnmnaatcncntgaagtn 991
 DB 841 gaacatgacgaatlaacacatctgtcgtcttcaatlaactcgttcaagtna 900
 OY 992 gntnancngngtgaacnctmnaatmtmngnngnngnngnngnngnngn 1051
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 DB 961 tatagaagaagatlaactgaactgaactgaactgaactgaactgaactgaact 1020
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 OY 1172 tnnatgcnmtlnmngnngnngnngnngnngnngnngnngnngnngn 1231
 DB 1081 tatagtcgcatgttacaagaatcgttgcgttatttaaacctattataaaccaatg 1140
 OY 1232 tannmmmtatannmncnlnaanaaannlnna 1263
 DB 1141 tataacattatagaacattaaanaacuaaa 1172
 RESULT 9
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 ID AAX37801 standard; DNA; 1283 BP.
 AC AAX37801:
 XX 09-JUL-1999 (first entry)
 DE Staphylococcus capitis Fema DNA.
 DE
 XX Fema; identification; detection; therapy; infection; femb;
 XX amplification; genotyping; gram-positive bacteria; vaccine; ss.
 OS Staphylococcus capitis.
 XX

[illegible]

Dh	361	ggccatgagctgagtttccatctaaagaaagaaatctaaagaaagagcttccat	420
Oy	455	amngcgtttgcacnctatmccaaagaaatmngtcmgtcgttccatctaaatctaaagaaagaa	514
Dh	421	aaagctctccatccatctctcaagaaagatactccgcttttgcgatttaaagaagataaa	480
Oy	515	amnnccnngantctttaaammnaagatctgattgntctttaaangnaaaagaaagaaagaa	574
Dh	431	acgcgctaaagctctcctcaagaaagagatgagtttaaagaagagctaaactaaagaaag	540
Oy	575	naaaaatagtgtaaaatctmnncttctmnnctmnnctmnnctmnnctmnnctmnnctmnn	634
Dh	541	naaaaatagtgtaaaatctmnncttctmnnctmnnctmnnctmnnctmnnctmnnctmnn	600
Oy	635	ctaaagaaagctctcmgc	694
Dh	601	cttaagaaagctctcctcaagaaagagtgctccgcgaataagagtaagctctctctctct	660
Oy	695	aamngctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnn	754
Dh	661	atgcgataaaatctctaaagaaagagatgattagctcctcaagctatgctgcttgcgt	720
Oy	755	gattctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnn	814
Dh	721	gattctcttgaagaaatctaaagaaagagatgctctctctctctctctctctctctctct	780
Oy	815	ctcaagaaatcttgcgaagaaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	840
Dh	781	ctcaagaaatcttgcgaagaaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	840
Oy	875	naaaacnctatmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnnctmnn	934
Dh	841	caacaaacatctgcagctcaacacacaaatctgcagagctcaaaactcctcaacagaa	900
Oy	935	catgaaagaagaatctcaac	994
Dh	901	catgaaagaagaatctcaac	960
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Dh	961	tattctmngctgc	1020
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Dh	1021	tggaaatcttgaatctaaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1080
Oy	1115	agtgatctaaatcttgaatctaaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1174
Dh	1081	agtgatctaaatcttgaatctaaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1140
Oy	1175	atgc	1234
Dh	1141	atgc	1200
Oy	1235	aaatctaaatcttgaatctaaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1294
Dh	1201	aaatctaaatcttgaatctaaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1260
Oy	1295	aaatctaaatcttgaatctaaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1354
Dh	1261	aaatctaaatcttgaatctaaatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1320
RESULT 10			
ID	AAK37799	standard: DNA: 1280 bp.	
AC	AAK37799:		
XX	09-JUL-1999 (first entry)		
Dh	Staphylococcus lugdunensis	FMDA DNA.	

DB 1261 agaaaggattatgcatgatcaaatctacagattaa 1297

RESULT 12
AAK37803 standard; DNK: 1284 BP.

AC AAK37803:
AT 09-JUL-1999 (first entry)
DE Staphylococcus sciuri FemA DNA.
FM FemA; identification: detection; therapy: infection; femB:
KM amplification; genotyping; gram-positive bacteria; vaccine: ss.
OS Staphylococcus sciuri.
FT Key Location/Dualifiers
TT 1..1284 A
CT /product= "FemA"
TT /note= "partial sequence, no start or stop codon"

PN MO9916780-AZ.
PD 08-APR-1999.
PX 28-SEP-1998: 98ND-BE00141.
PR 25-SEP-1997: 97EP-0870146.
PA (BENA-) BELGIAN MIN NAT DEFENCE.
PA (DTLO) ONIV CATHOLIQUE LOUVAIN.
XX Gala J. Vannuffel P.
XX MPI: 1999-287521/24.
DR P-PSDB: AA108320.
XN New Staphylococcus-specific oligonucleotides

XS Claim 25: Fig 11a-b: 48pp: English.

CC This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC detect products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococcal species.
CC Since the femA sequence also can be used for the molecular genotyping of
CC genes of different Staphylococci species or other gram-positive bacteria,
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.

SO Sequence 1284 BP: 518 A: 181 C; 215 G; 370 T; 0 Other:

Local Match 40.5% SCORE 537.6; DB 20: Length 1284;
Best Local Similarity 48.7% Pred. No. 2,3e+01;
Matches 634; Conservative 0; Mismatches 634; Indels 4; Gaps 2

OT gatttgggaatttcataaataaacgcgtcgcgcgtccattaccacaacgtagatat 56
DB 7 gaatttgagaatttcataaataaacgcgtcgcgcgtccattaccacaacgtagatat 56
OY 104 taaganaahaaantttcganannnnnmgamcnctagngatnaaanaanaat 153
DB 67 tatgaataaaaaaacatcgaaagtactcaacacacattagagagagccaagatcacaa 126

[illegible]

[illegible]

100

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Query Match      18.6%; Score 247.4; DB 4; Length 453;
Best Local Similarity 57.1%; Pred. No. 1.2e-52;
                   0 Mismatches 104; Gaps 0;
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7
RESULTS
US/95-265-315-6
: Sequence 6, Application US/09265315
: Patent No. 6187341
: GENERAL INFORMATION:
: APPLICANT: Benton, Bret
: APPLICANT: Lee, Ving J.
: APPLICANT: Malouin, Francois
: APPLICANT: Merlino, Matthew A.
: APPLICANT: Smith, Douglas B.
: APPLICANT: Sun, Douglas
: APPLICANT: Sun, Douglas
: TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
: TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
: TITLE OF INVENTION: TARGET GENES
: NUMBER OF SEQUENCES: 111
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C., DOS 5.0
: SOFTWARE: Microsoft 5.1
: APPLICATION DATA:
: APPLICATION NUMBER: US/09/265,315

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NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Suite 4700
 STATE: Los Angeles
 COUNTRY: U.S.A.
 ZIP: 90071-2056
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 PRIORITY NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-6

FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-6

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 Best Local Similarity 55.9% Pred. No. 2e-47
 Matches 229 Conservative 0 Mismatches 181 Indels 0 Gaps 0
 Oy 675 gngagannnttntantanaannntnnnnnnattnnaaagannnnngntngnncnn 734
 Db 1 GTAAAGCAAAATTAACCTACACCTGCTTAAATATATACAAAGACCGCTGTGACCTT 60
 Oy 735 tngctatantnttgatgattantnnnnngannnnnnnnnnnnnnnnnnnnnnnn 794
 Db 61 TAGCGTATATCACTTTATGATATATATTAAGAACTAAAGAGCGGTATATTTAA 120
 Oy 795 ntaagannnnnaaagannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 854
 Db 121 ATAAAGTTTAAATTAAGCGTTAAAGGATATTAAGAACTGCTGAAATATAAAGAC 180
 Oy 855 nnaaann 914
 Db 181 ATAAAGCGAGATAACTTACAAACAACTTGTGCAATGAGCAAAAGATTGACAG 240
 Oy 915 nnaann 974
 Db 241 GTAAGCGTACAGAGCAACATGTAATGATTAACCTATCTCTCTGTTCTTCTTA 300
 Oy 975 tnaatcctntgaatgattantnnnnngannnnnnnnnnnnnnnnnnnnnnnnnn 1034
 Db 301 TCAATCCATTGANGTGTATATATGCTGTGATACAAATGCAATGCTGCTCAATT 360
 Oy 1035 cngnagntatgcnntcnaatgannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1084

Query Match 17.0% Score 226.2 DB 4 Length 410
 Best Local Similarity 55.9% Pred. No. 2e-47
 Matches 229 Conservative 0 Mismatches 181 Indels 0 Gaps 0
 Oy 675 gngagannnttntantanaannntnnnnnnattnnaaagannnnngntngnncnn 734
 Db 1 GTAAAGCAAAATTAACCTACACCTGCTTAAATATATACAAAGACCGCTGTGACCTT 60
 Oy 735 tngctatantnttgatgattantnnnnngannnnnnnnnnnnnnnnnnnnnnnn 794
 Db 61 TAGCGTATATCACTTTATGATATATATTAAGAACTAAAGAGCGGTATATTTAA 120
 Oy 795 ntaagannnnnaaagannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 854
 Db 121 ATAAAGTTTAAATTAAGCGTTAAAGGATATTAAGAACTGCTGAAATATAAAGAC 180
 Oy 855 nnaaann 914
 Db 181 ATAAAGCGAGATAACTTACAAACAACTTGTGCAATGAGCAAAAGATTGACAG 240
 Oy 915 nnaann 974
 Db 241 GTAAGCGTACAGAGCAACATGTAATGATTAACCTATCTCTCTGTTCTTCTTA 300
 Oy 975 tnaatcctntgaatgattantnnnnngannnnnnnnnnnnnnnnnnnnnnnnnn 1034
 Db 301 TCAATCCATTGANGTGTATATATGCTGTGATACAAATGCAATGCTGCTCAATT 360
 Oy 1035 cngnagntatgcnntcnaatgannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 1084
 Db 361 CCGAGATTATGCGTAAATGCGAAATGATTATATGCTGATTAAATCAAT 410

RESULT 8
 US-09-265-315-6
 Sequence 6, Application US/09265315
 Patent No. 6183333
 GENETIC INFORMATION:
 APPLICANT: Benlon, Bret
 APPLICANT: Lee, Ying J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martio, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE OR INACTIVE COMPOUNDS
 TITLE OF INVENTION: TARGET GENES

```

361 CCGGAGCTTATGCAGTCGATCGGAATGGMAATGATTAAATTATTCGCAATTAAATCAT 410

RESULT      9
US-09-266-417-6
: Sequence 6, Application US/09266417
: Patent No. 6228588
: GENERAL INFORMATION:
: APPLICANT : Benton, Bret
: APPLICANT : Lee, Ying J.
: APPLICANT : Marzulli, Nicholas
: APPLICANT : Martin, Patrick R.
: APPLICANT : Schmid, Molly B.
: APPLICANT : Sun, Dongxu
: TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
: TITLE OF INVENTION: ACTION ON STAPHYLOCOCCUS AUREUS
: NUMBER OF SEQUENCES: 111
: COMMENTARY: NO CROSS-III
: ADDRESSER: LYON & LYON
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2086 TORN:
: COMPUTER MODEL: 3.5" Diskette, 1.44 MB
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA: US/09266.417
: APPLICATION NUMBER: US/09266.417
: FILING DATE: September 9, 1999
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/714,918
: FILING DATE: September 13, 1996
: APPLICATION NUMBER: 60/009,192
: FILING DATE: December 22, 1994
: APPLICATION NUMBER: 60/001,798
: FILING DATE: September 15, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 240/248
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 955-0400
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 410 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: ORIENTATION: linear
US-09-266-417-6

Query Match          17.0% Score 226.2 DB 4 Length 410:
Best Local Similarity 55.9% Pred. No. 2e-47:
Matches 229: Conservative 0 Mismatches 181 Indels 0 Gaps 0

Oy 675 cggagcgmnttctatanaangntnnnnnnaaaanngnngntngttccnn 934
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GTATGACCAATTTAAGTACATACGCCCTTAAAATATTACAAGACGCTGTGNAGTACCII 60

Oy 735 tgcgtctatatanttgtagtcantntnnngantntnnngannngannnnnnntaa 794
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 61 TAGCGTATATACACTTTTATTCGATATATTAAAGAACATAAGACGCGTGATATTITAA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 795 ctacaaaanataaacgcntnnaangnatnnganaaangncgccnganaaaaaaangcn 924
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

1 GENERAL INFORMATION:
2 APPLICANT: Benton, Bret
3 APPLICANT: Lee, Ying J.
4 APPLICANT: Matoulin, Francois
5 APPLICANT: Martin, Pellicier K.
6 APPLICANT: Schmitt, Doreen
7 APPLICANT: Schmitt, Douglas
8 TITLE OF INVENTION: METHODS ON
9 TITLE OF INVENTION: TARGET GEN
10 NUMBER OF SEQUENCES: 111
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Lyon & Lyon
13 STREET: 633 West Fifth Street
14 STREET: Suite 4700
15 CITY: Los Angeles
16 STATE: California
17 COUNTRY: U.S.A.

FILING DATE: De

REPORT TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: 3.5" Diskette
 MEDIUM TYPE: 3.5" Diskette
 OPERATING SYSTEM: IBM PC, DOS 5.0
 SOFTWARE: Word Perfect 5.1
 PRESENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 FOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: 11, 1995
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798


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GenCore version 4.5
Copyright (C) 1993 - 2000 CompuGen Ltd.

ROM nucleic - nucleic search, using sw model

June 20, 2002, 09:31:30 : Search time 8551.36 Seconds
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Title: US-09-509-234C-1
Perfect score: 1328
Sequence: 1 nnnnnnnnnnnnaatga.....gaaattacaggttaanna 1328

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:      13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters:    27472414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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ORIGIN

10


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Best Local Similarity 25.4%; Pred. No. 0.02;
Matches 115; Conservations 20; Mismatches 308; Indels 0; Gaps 0;

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[illegible]

DB 451 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 478
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RESULT 6
CNSOLJRG/c
LOCUS
DEFINITION
Anopheles gambiae GSS 17 end of clone 14007 from panel library
from Anopheles gambiae (African malaria mosquito),
containing complete genome sequence.
GSS 12-JUN-2001

genomic survey sequence.

Accession
Number
AL147405.1 GI:7005551
Keywords
GSS
Organism
African malaria mosquito.
Anopheles gambiae
Anopheles gambiae
Arachnida: Mesoseta; Tracheata: Hexapoda; Insecta:
Terygota; Endopterygota; Diptera; Nematocera.
Culture; Anophelinae
Cultured; 1 (bases 1 to 879)

FEATURES	Location/Qualifiers
COMMENT	Roux, Paris 75015, France This clone is from an <i>A. gambiae</i> BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

Oy 1169 ggnatnngcngantntngantngtngtngantntntnaacncntnaaancn 1288
 Db 727 TTTATTTTAAATATATATATATATATATATATATATATATATATATAT 1286
 Oy 1229 nctatnn 1288
 Db 767 ATTAT 846
 Oy 1289 naann 1320
 Db 847 AAAATTTTATATATATATATATATATATATATATATATATATAT 878

RESULT 8
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 LOCUS ENTER310TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
 DEFINITION genomic, DNA sequence.
 A2548467
 ACCESSION A2548467.1 GI:1172102
 VERSION
 KEYWORDS
 SOURCE Entamoeba histolytica.
 ORGANISM Entamoeba histolytica.
 Entamoeba histolytica: Eukaryota; Eukaryota; Entamoebidae; Entamoeba.
 REFERENCE 1 (bases 1 to 908)
 Loftus, B., Van Aken, S. and Fraser, C.
 Determination of clone end sequences from Entamoeba histolytica
 HMI:IMSS sheared DNA library
 UNPUBLISHED (2000)
 CONTACT: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9741 Rockville Pike
 Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjl@fustig.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
 DNA library
 Seq primer: M13-Reverse
 Class: shotgun
 High quality sequence start: 17
 High quality sequence end: 878.
 High quality region/Qualifiers
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 /organism="Entamoeba histolytica"
 /strain="HMI:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pBOS1; Site 1: Best 1; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA was sheared by sonication and ligated into
 pBOS1 vector. The library was constructed by Clark and Diamond (Clark,
 C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a
 method for isolate identification. Exp. Parasitol.
 77:450.). The DNA was mechanically sheared to give a
 tight size distribution (~2 kb). The v + i method used for
 the library construction is described in detail in Smith,
 H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing projects. In Genome
 Sequencing: A Practical Approach, Vol. 1, Oxford University Press, 1999)."
 434 a 16 c 289 g 169 t

BASE COUNT 434 a 16 c 289 g 169 t

Query Match 5.11: Score 67.6; DB 12: Length 908;
 Best Local Similarity 26.54; Pred.No.0.044;
 Matches 193; Conservative 0; Mismatches 534; Indels 0; Gaps 0;

Oy 251 gattntnaaannagantngtntntnttttaagantntnnnaantatntnaa 310
 Db 151 GATGAGATGATGAGACGCAATATGATGATGATGATGATGATGATGATG 210

Oy 311 pannaannnt 370
 Db 211 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 270
 Oy 371 gangngantntnnngntaagcngnngnangattgntntngatntntntnnnnnn 430
 Db 271 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 330
 Oy 431 ggnntnancnngntntnnnnngntntgancntntnnnnnnnnnnnnnnnn 490
 Db 331 GAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 390
 Oy 491 tngnt 550
 Db 391 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 450
 Oy 551 ggnnngntnaacnaaaagcngnngntntntntntntntntntntntntnt 610
 Db 451 GAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 510
 Oy 611 gannnt 670
 Db 511 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 570
 Oy 671 gntngnt 730
 Db 571 GAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 630
 Oy 731 cngnt 790
 Db 631 GAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 690
 Oy 791 nLnantaagannnnnaaaagcngntntnaangntnaangntnaangntna 850
 Db 691 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 750
 Oy 851 gcnmnaaann 910
 Db 751 GATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 810
 Oy 911 gann 970
 Db 811 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 870
 Oy 971 ntntna 977
 Db 871 AAAATGA 877

RESULT 9
 CNS03NVO 984 bp DNA linear GSS 17-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
 DEFINITION 040808 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 AL252575.1 GI:7973587
 CNS03NVO/c Tetraodon nigroviridis genome survey sequence.
 Tetraodon nigroviridis
 Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
 Tetraodontidae; Tetraodon.
 1 (bases 1 to 984)
 Jaillon, O., Dasilva, C., Fizanes, C., Fisher, C.,
 Roest-Crolius, H., Litalien, A., Quetier, F., Saurin, M., Bernot, A. and
 Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 UNPUBLISHED
 2 (bases 1 to 984)
 Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Qy	622	aaatnnatgntcatatgatgagataccnngannnnaangntnnnnngatngangaga	691
Ds	483	tgatgatgatgatgagagagagatgatgatgatgatgagagagagatgatgatgagatga	541
Qy	682	nnnnntatanaangntnnnnnaatttnaaagannngntnnlgttccnntngccta	741
Ds	542	tgatgagagagagatgagagagatgatgagagagatgatgagagatgatgagagagag	601
Qy	742	catnnanttttgatgattnnnnnngatnnnnnnnngannnnnnnnnnnnnnnnnnaaaga	801
Ds	602	agagagatgatgatgagagagatgatgagagagatgagagagagatgatgatgagagatga	661
Qy	802	nnnnnaaaagatnnnaagatnnnaagatnnnaagatnnnaagatnnnaagatnnnaagaa	861
Ds	662	tgatgagagagagatgatgatgagagagatgatgagagagagatgatgatgagagatgatga	721
Qy	862	nnnnnnnaaantnnnaaantnnnnngnnnaannnaaaantnnnangnnnnnnnnnn	921
Ds	722	agagagagatgagagatgatgatgagagagagatgagagagatgatgatgagagagagatga	781
Qy	922	nnnnnnnnnaaantgnaaaga	946
Ds	782	tgatgagagagagatgagagagagatgagagagagatgagagagagatgagagagag	806

RESULT	11
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LOCUS	781 bp DNA linear GSS 01-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TE13 end of BAC #
DESCRIPTION	BACR19009 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	U053444
VERSION	1
KEYWORDS	GSS
SOURCE	GI:4934889
ORGANISM	fruit fly
REFERENCE	Drosophila melanogaster
AUTHORS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
JOURNAL	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
COMMENT	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila;
	1 (bases 1 to 781)
	Genoscope
	Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
	Determination of this BAC-end sequence was carried out as part of a
	collaboration with The Berkeley Drosophila Genome Project (BDGP).
	The BDGP is constructing a physical map of the Drosophila
	melanogaster genome using these BACs. For further information
	please see http://www.fruitfly.org the BDGP Drosophila
	melanogaster BAC library in Placerville, CA. The J. G. P.'s laboratory is the Department of
	Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
	NY. The library is named RPCI-98 and was constructed by partial
	EcoRI digestion of Drosophila DNA provided by the BDGP from the
	isogenic strain Y2; cn bw. The same strain used for the BDGP's
	P1 and EST libraries. A more detailed description of the library
	and how to order individual BAC clones, the entire library, or
	filters for hybridization from the BACPAC Resource Center can be
	found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .
FEATURES	Location/Qualifiers
source	1..781
	/organism="Drosophila melanogaster"
	/db_xref="taxon:7227"
	/clone_lib="RPCI-98"
	/clone="BACR19009"
	/note="end : TE13"
BASE COUNT	440 a 71 c 6 g 189 t 75 others
ORIGIN	

Query Match	5.0%	Score 67	DB 12	Length 781
Best Local Similarity	27.9%	Pred. No. 0.056		

Matches	140:	Conservative	13:	Mismatches	348:	Indels	0:	Gaps	0:
Oy	495	tnttattatntnnnnnaaaacnncnngentntntnaannnalgatngntngna	554						
Db	55	WTTTAAATTTAAAAATATAAAAWAAATATAAAATTTAATTAATAAAATTTATATNAAT	114						
Oy	555	angngnaancnaaaagntnnnaanaagtcngncaagtcnntntntnnnaagng	614						
Db	115	AAAAAATATATAAAATATATAAAWAAATATATAAAWAAATATAAAWAAWAA	174						
Oy	615	antncnccatnttngnttcattgaagatacncnccnccnccnccnccnccnccn	674						
Db	175	AAAAAATAAAAAAATAAAATTTATTAATAAAAAAATAAAATTTAAATATAATAAA	234						
Oy	675	gngangannntntntanaangntnnnnnatntnaaagannngtntngtuccnn	734						
Db	235	TAATAAAATAAAATATATAAATTTTAAATTTTAAATTTTAAATTTATTTAAATTTAA	294						
Oy	735	ngctatacnnnttggatcannnnnnngnngnngnngnngnngnngnngnngn	794						
Db	295	AAAAATTAATAAAATATAAAWAAATATAAAWAAATATAAAWAAATATAAAWAA	354						
Oy	795	ntaaagannnaaaagcnnnaangnngatngnnaaagcngcngcngcngcngcng	854						
Db	355	AAAAAATAAAAAAATAAAATTTATTAATAAAATTTTAAATTTTAAATTTTAAATTTAA	414						
Oy	855	nnnaaannnnnnnaantnnnaancnccnccnccnccnccnccnccnccnccnccn	914						
Db	415	AAAAATTAATTTAAAAAATATAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA	474						
Oy	915	nnnnnnnnntnnnaannnccnccnccnccnccnccnccnccnccnccnccnccnccn	974						
Db	475	TAATAATAAAATAAATAAACAAAAAATAATTAATAAAATTTAATAATTTTAAATTTAA	534						
Oy	975	ntaatcctntgaagtcngtnt	995						
Db	535	TAATAAAATAAACACGCGTCB	555						

RESULT 12

AS2546009/C

LOCUS

DEFINITION

ENTF533F Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000 genomic, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AS2546009

ENTF533F

AS2546009.1

GI:11167130

GSS

Entamoeba histolytica

Entamoeba histolytica

1 (bases 1 to 849)

Loftus,B., Van Aken,S. and Fraser,C.

Determination of clone end sequences from Entamoeba histolytica

HMI:IMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

NIH Intramural Research Program

9750 Rockville Pike, Room 3D10

Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b.loftus@nih.gov

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library

Seq primer: M13-Forward

Class: shotgun

High quality sequence start: 26

High quality sequence stop: 795

High quality sequence length: 849

Location/Qualifiers

1..849

/organism="Entamoeba histolytica"

/strain="HMI:IMSS"

/db_xref="taxon:5759"

FEATURES

source

AZ693582.1 GI:11820728
 GSS.
 Entamoeba histolytica.
 Entamoeba histolytica.
 Entamoeba histolytica.
 Eukaryota; Entamoebidae; Entamoeba.
 1 (bases 1 to 891)
 Loftus.B., Van Aken.S. and Fraser.C.
 Determination of clone end sequences from Entamoeba histolytica
 JMI:IMSS sheared DNA library
 Unpublished (2000)
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The University of Guelph, Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: b.loftus@lar.org

DNA library
Seq primer: M13-Reverse
Class: Shotgun
High quality sequence start: 16
High quality sequence stop: 694.

FEATURES

source	High quality sequence	SCOP: 094.	Localism/Qualifiers
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			/strain="IMJ: IMSS"
			/db_xref="taxon:5759"
			/clone_lib="Entamoeba histolytica Sheared DNA"
			/note="Vector: pHSI1: Site_1: Bst I: Constructed at the Institute for Genomic Research (IGR), Rockville, MD. Genomic DNA isolated from brocth and diamond (Clark, C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing. Pacific Biosciences, Inc. Oxford University Press, 1999)."
			Bartel, S.S. C. 291.g. 145 t.
			400 a
			BASE COUNT

Query Match	5.0%	Score 56.4	DB 12	Length 891
Percent Similarity	26.6%	Pred. 0	0.07	
Matches 175	Conservative	0	Mismatches 483	Indels 0
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Db	33	AAGATGATGATGAAGATGATTATGATGAAGATGATGAATTTGATTAGACGACGATG	92	
Oy	348	ttnctatcatannnaatcagagagagatnnnnnaaagcagcagcnnnaagattggn	40	
Oy	93	ANGATGATGAAGATGATGATGATGACGATGATGATGAAGACGATGATG	152	
Oy	408	lntntaannntnnnnnnntngntntnaannnnngntnnnnnnngntllganc	467	
Db	153	AAGAAGATGATGATGAAGAAGATGATGATGAAGAAGATGATGATGAAGATGATG	212	
Oy	468	cnntnnncbaatngntntncatntngntlnatntlnnnnnnaaannnnnncan	527	
Db	213	ATGAAGATGACGATGATGATGAAGAAGATGATGATGACGATGAAGACGATGAAGAAG	272	
Oy	528	tntntnaannnatggatngntnngaannnnaacnaaaagntnnnaanaatgng	587	
Db	273	ACGATGAAGAAGACGATGAAGAAGACGATGAAGAAGACGATGAAGACGATGAAGAAG	347	
Oy	588	tnaaagttnnnltnntnnnnnaaaagcagcctnncaatntngntcattatgagacga	632	
Db	333	ACGATGATGATGATGAAGAAGACGATGATGATTTGATTAGAAGACATGATG	392	

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Oy 648 cncgagannncgannntnnngatnggngannnnntntntanaaangntnnnnnnnnnn 707
Db 393 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATG 452
Oy 708 attnaaagannntngntngcncntatntnnnttngatntnnnnnnnnnnnnnnnn 767
Db 453 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATG 512
Oy 758 aattnnannnnngannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 827
Db 513 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATG 572
Oy 828 aanaagcncnnaaanaaanaaangcnnnaaannnnnnnnnnnnnnnnnnnnnnnn 887
Db 573 AAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATG 932
Oy 888 nngcnaannncnaaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 945
Db 633 ATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATGATGAAGAGACGATG 950

RESULT 14
CNS0183Y
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence SF6 end of BAC
BACN37F08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL108856.1 GI:5629160
VERSION
KEYWORDS
SOURCE
ORGANISM
fruit fly,
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
Genoscope.
AUTHORS
Direct Submission
JOURNAL
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 951 91006 EVRY cedex FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBAC11.
FEATURES
Location/Qualifiers
source
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="drosBAC"
/clone="BACN37F08"
/note="end : SP6"
BASE COUNT 465 a 25 c 90 g 204 t 317 others
ORIGIN

Query Match 5.0%; Score 66.2; DB 12; Length 1101;
Best Local Similarity 23.9%; Pred. No. 0.074;
Matches 162; Conservative 53; Mismatches 461; Indels 1; Gaps 1;

Oy 542 gctgntnnngannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 501
Db 178 KATGGGAGGAGGATGGGGATAGAAATGKTTTCGATAGTGGGAGGANNNAANTTT 237
Oy 602 ntannnnnnaagannntcncntntnnngcncatntatngatngatcncngcnnnaa 561
Db 238 KKATAAGNNKNGNNAANAATAATTAATAAATAAATAAATAAATAAATAAATAAATA 297

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Search completed: June 20, 2002, 14:26:42
Job time: 17712 sec